Serial No. 10/789,831

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NEWS 6 SEP 11 CA/CAplus enhanced with more pre-1907 records
NEWS 7 SEP 21 CA/CAplus fields enhanced with simultaneous left and right truncation
NEWS 8 SEP 25 CA(SM)/CAplus(SM) display of CA Lexicon enhanced
NEWS 9 SEP 25 CAS REGISTRY(SM) no longer includes Concord 3D coordinates
NEWS 10 SEP 25 CAS REGISTRY(SM) updated with amino acid codes for pyrrolysine
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NEWS 14 OCT 23 Option to turn off MARPAT highlighting enhancements available
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NEWS 18 NOV 03 JAPIO enhanced with IPC 8 features and functionality
NEWS 19 NOV 10 CA/CAplus F-Term thesaurus enhanced
NEWS 20 NOV 10 STN Express with Discover! free maintenance release Version 8.01c now available
NEWS 21 NOV 13 CA/CAplus pre-1967 chemical substance index entries enhanced with preparation role

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FULL ESTIMATED COST 0.21 0.21

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FILE COVERS 1907 - 15 Nov 2006 VOL 145 ISS 21
FILE LAST UPDATED: 14 Nov 2006 (20061114/ED)

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E2 1 YGUARAN F R ALVAREZ/AU
E3 0 --> YGUERABIDE/AU
E4 1 YGUERABIDE E E/AU
E5 2 YGUERABIDE EVANGELINA/AU
E6 8 YGUERABIDE EVANGELINA E/AU
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E8 1 YGUERABIDE JAUN/AU
E9 50 YGUERABIDE JUAN/AU
E10 1 YHAN VAAGUE I/AU
E11 1 YHANG SOOK YOUNG/AU
E12 1 YHANG YANWAN/AU

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L1 59 ("YGUERABIDE E E"/AU OR "YGUERABIDE EVANGELINA"/AU OR "YGUERABID E EVANGELINA E"/AU OR "YGUERABIDE J"/AU OR "YGUERABIDE JAUN"/AU OR "YGUERABIDE JUAN"/AU)

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L2 58 L1 NOT 2006/PY

=> s l2 not 2005/py 1364069 2005/PY
L3 54 L2 NOT 2005/PY

=> s l3 not 2004/py 1322140 2004/PY
L4 52 L3 NOT 2004/PY

=> s l4 not 2003/py 1261103 2003/PY
L5 50 L4 NOT 2003/PY

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L6 0 L5 AND (PARTICULATE (A) LABEL#)/BI,AB

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L7 0 L5 AND PARTICULATE/BI,AB

=> s l5 and hybridi?/bi,ab 176832 HYBRIDI?/BI 151042 HYBRIDI?/AB
L8 3 L5 AND HYBRIDI?/BI,AB

=> d l8 1-3 bib ab

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:127318 CAPLUS <<LOGINID::20061115>>
DN 136:228894
TI Resonance light scattering particles as ultrasensitive labels for detection of analytes in a wide range of applications
AU ***Yguerabide, Juan*** ; ***Yguerabide, Evangelina E.***
CS Genicon Sciences Corporation, San Diego, CA, USA
SO Journal of Cellular Biochemistry (2001), (Suppl. 37), 71-81 CODEN: JCEBD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal
LA English
AB We have developed a new detection technol. that uses resonance light scattering (RLS) particles as labels for analyte detection in a wide range of formats including immuno and DNA probe type of assays in soln., solid phase, cells, and tissues. When a suspension of nano sized gold or silver particles is illuminated with a fine beam of white light, the scattered light has a clear (not cloudy) color that depends on compn. and particle size. This scattered light can be used as the signal for ultrasensitive analyte detection. The advantages of gold particles as detection labels are that (a) their light producing power is equiv. to more than 500,000 fluorescein mols., (b) they can be detected at concns. as low as 10-15 M in suspension by eye and a simple illuminator, (c) they do not photobleach, (d) individual particles can be seen in a simple student microscope with dark field illumination, (e) color of scattered light can be changed by changing particle size or compn. for multicolor multiplexing, and (f) they can be conjugated with antibodies, DNA probes, ligands, and protein receptors for specific analyte detection. These advantages allow for ultra-senstive analyte detection with easiness of use and simple and relatively inexpensive instrumentation. We have shown that our RLS technol. can indeed be used for ultra-sensitive detection in a wide range of applications including immuno and DNA probe assays in soln. and solid phases, detection of cell surface components and in situ ***hybridization*** in cells and tissues. Most of the assay formats described in this article can be adapted for drug fast throughput screening.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:645343 CAPLUS <<LOGINID::20061115>>
DN 125:294164
TI Pyrene-labeled DNA probes for homogeneous detection of complementary DNA sequences: poly(C) model system
AU ***Yguerabide, Juan*** ; Talavera, Eva; Alvarez, Jose Maria; Afkir, Moustafa
CS Department of Biology, Univ. of California, San Diego, La Jolla, CA, 92093, USA
SO Analytical Biochemistry (1996), 241(2), 238-247 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic
DT Journal
LA English
AB DNA and RNA probes are important anal. reagents in mol. biol. and in the detection of infectious and genetic diseases. However, the present polynucleotide probe technol. is complex and labor-intensive. We have been investigating the possibility of using fluorescent-labeled DNA probes to develop assays which do not require the sepn. of free from ***hybridized*** probe (homogeneous assays). Such assays are possible if the fluorescence efficiency or fluorescence anisotropy of the fluorescent label changes upon ***hybridization*** of probe with target DNA. In this article we examine pyrene as a fluorescent label for DNA or RNA probes. Expts. were performed using a model system in which poly(C) and poly(I) are resp. the probe and target sequences. A small fraction of the nucleotide bases of poly(C) was randomly labeled with pyrene using the bisulfite-catalyzed diamine reaction. The results show that the uncorrected emission spectrum of pyrene-poly(C) decreases by a factor of 4 and shifts toward longer wavelengths upon ***hybridization*** with poly(I) at satg. concns. The av. lifetime changes from 10.78 to 4 ns. These fluorescence changes occur in a wide range of chem. environments, including the high salt concns. normally used to increase the velocity of the ***hybridization*** reaction in clin. assays. The pyrene label can thus be used to readily detect the amt. of poly(I) in an unknown sample without having to sep. free and bound labeled probe. To unravel the mechanism responsible for the obsd. changes in fluorescence intensity upon ***hybridization*** , we have performed polarized fluorescence intensity measurements and analyzed the results by approx. steady-state expressions that allow evaluation of the relative contributions of changes in lifetimes (fluorescence efficiency) and rotational motions to the changes in fluorescence intensity. The results indicate that the latter changes are due chiefly to changes in lifetime or fluorescence efficiency and that these changes seem to be due to the movement of the pyrene label to a more hydrophilic environment upon ***hybridization*** .

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:711884 CAPLUS <<LOGINID::20061115>>
DN 123:134230
TI Quantitative fluorescence method for continuous measurement of DNA ***hybridization*** kinetics using a fluorescent intercalator
AU ***Yguerabide, Juan*** ; Ceballos, Antonio
CS Dep. Biol., Univ. California San Diego, La Jolla, CA, 92093, USA
SO Analytical Biochemistry (1995), 228(2), 208-20 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic

DT Journal
LA English
AB A quant. fluorescence method is presented for continuous measurement of DNA or RNA ***hybridization*** (including renaturation) kinetics using a fluorescent DNA intercalator. The method has high sensitivity and can be used with reaction vols. as small as 1 .mu.L and amts. of DNA around 1 ng. The method is based on the observations that (i) for the usual ***hybridization*** conditions, intercalators such as ethidium bromide bind (intercalate) to double-stranded DNA (dsDNA) but not single-stranded DNA or RNA and (ii) there is a large increase in fluorescence intensity when intercalators such as ethidium bromide bind to dsDNA. In this application, the intercalator can be considered as a quant. indicator of dsDNA concn. When a small amt. of intercalator is added to a ***hybridizing*** soln., the fluorescence intensity of the intercalator increases with increase in dsDNA. The ***hybridization*** reaction can thus be monitored by continuously recorded fluorescence intensity vs. time. Because the amt. of intercalator bound to dsDNA is not necessarily proportional to dsDNA concn., the time-dependent fluorescence intensity graph is not identical to the kinetic graph [dsDNA] vs. t. However, the fluorescence intensity vs. time graph can easily be converted to the true [dsDNA] vs. t graph by an exptl. calibration graph of fluorescence intensity vs. [dsDNA]. This calibration graph is obtained in a sep. expt. using samples contg. known amts. of dsDNA in the ethidium bromide buffer used in the kinetic measurement. Exptl. tests of the intercalator technique are provided using ethidium bromide as an intercalator and DNA from Escherichia coli and .lambda.-phage and poly(I)-poly(C) RNA hybrids. These DNA and RNA samples have Cot1/2 values that cover a range of 106. The exptl. results show that (i) the kinetics of ***hybridization*** are not significantly perturbed by the intercalator at concns. where no more than 10% of the binding sites on DNA or RNA hybrids are occupied, (ii) the kinetic graphs obtained by the intercalator fluorescence method and cor. with the calibration graph agree with kinetic graphs obtained by optical absorbance measurements at 260 nm, and (iii) the intercalator technique can be used in the different salt environments often used to increase the velocity of the ***hybridization*** reaction and at the ***hybridization*** temps. (35-75.degree.) normally used to minimize nonspecific ***hybridization*** .

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YGUERABIDE/AU
L1 59 S E4-E9
L2 58 S L1 NOT 2006/PY
L3 54 S L2 NOT 2005/PY
L4 52 S L3 NOT 2004/PY
L5 50 S L4 NOT 2003/PY
L6 0 S L5 AND (PARTICULATE (A) LABEL#)/BI,AB
L7 0 S L5 AND PARTICULATE/BI,AB
L8 3 S L5 AND HYBRIDI?/BI,AB

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TOTAL ENTRY SESSION
FULL ESTIMATED COST 46.08 46.29

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FILE TOTAL ENTRY
SESSION
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EAST Search History

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L1	258	hybridi$ near20 nanoparticle	US-PGPUB; USPAT	OR	ON	2006/11/15 16:04
L2	34859	435/6[ccls]	US-PGPUB; USPAT	OR	ON	2006/11/15 16:04
L3	184	l1 and l2	US-PGPUB; USPAT	OR	ON	2006/11/15 16:04
L4	1180839	@rlad<"20030227"	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L5	120	l3 and l4	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L6	398490	@pd>"20060127"	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L7	8	l5 and l6	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L8	8463	polya	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L9	22978	poly adj "a"	US-PGPUB; USPAT	OR	ON	2006/11/15 16:05
L10	1569	poly adj adenyl$	US-PGPUB; USPAT	OR	ON	2006/11/15 16:06
L11	27917	l8 or l9 or l10	US-PGPUB; USPAT	OR	ON	2006/11/15 16:06
L12	97	l1 and l11	US-PGPUB; USPAT	OR	ON	2006/11/15 16:06
L13	92	l2 and l12	US-PGPUB; USPAT	OR	ON	2006/11/15 16:06
L14	82	l4 and l13	US-PGPUB; USPAT	OR	ON	2006/11/15 16:06

EAST Search History

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L1	28849	polya or (poly adj "a") or (poly adj adenyl$)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:05
L2	960457	array$ or microarray$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:05
L3	10880	l1 and l2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:05
L4	1180839	@rlad<"20030227"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:05
L5	7233	l3 and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:06
L6	880	(polya or (poly adj "a") or (poly adj adenly$)) same (array$ or microarray$)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:07
L7	593	l4 and l6	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 17:07

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L1	11	oligodt near10 prob$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:00
L2	728	(oligo near10 dt) near10 (probe or probed or probing)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:01
L3	730	l1 or l2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:01
L4	1180839	@rlad<"20030227"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:02
L5	544	l3 and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:02
L6	325	l5 and (array$ or microarray$)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:02
L7	182	l6 and 435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/15 18:02

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151042 HYBRIDI?/AB          72446 NANOPARTICLE#/BI
49729 NANOPARTICLE#/AB
L1        479 (HYBRIDI?(20A)NANOPARTICLE#)/BI,AB

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POLY/BI          484421 POLY/AB          20336303 A/BI
19747296 A/AB          18754 POLY(W)A    684462 POLY/BI
484421 POLY/AB          60081 ADENYL?/BI
45965 ADENYL?/AB          461 POLY(W)ADENYL?
L2       20113 ((POLYA) OR (POLY(W)A) OR
(POLY(W)ADENYL?))/BI,AB

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L3          2 L1 AND L2

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L3 2 S L1 AND L2

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L3 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2006:657191 CAPLUS <<LOGINID::20061115>>
DN 145:79273
TI Methods and apparatus for SERS assay of biological analytes using oligonucleotide probes labeled with composite org.-inorg. nanoparticles (COIN)
IN Su, Xing
PA Intel Corporation, USA
SO U.S. Pat. Appl. Publ., 36 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 2006147941 A1 20060706 US 2004-26857 20041230
PRAI US 2004-26857 20041230
AB SERS technol. is used for high throughput screening of biol. analytes and samples. For polynucleotide sequencing, sets of oligonucleotide probes are labeled with composite org.-inorg. nanoparticles (COIN) that produce distinguishable SERS signals when excited by a laser. Detection of a hybridization complex contg. members of two such COIN-labeled probe sets will reveal a 12 nucleotide sequence segment of the target polynucleotide. Also provided are surface-modified arrays and chips with multiple arrays to which sets of probe-conjugated COIN or other reporter substrates are immobilized. Analytes are detected by contacting a sample, such as a bodily fluid, with the array-anchored probes. Captured analytes are tagged with an addnl. target-specific Raman-active tag. Two or more Raman signatures emanating from the detection complexes reveal the identity of the captured analytes.

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:14610 CAPLUS <<LOGINID::20061115>>
DN 142:108381
TI Quantitation of individual mRNAs in gene expression profiling by microarray ***hybridization*** with oligo-(dT) probes conjugated to ***nanoparticles***
IN Bao, Yijia P.; Mueller, Uwe R.
PA Nanosphere, Inc., USA
SO PCT Int. Appl., 54 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2005001143 A2 20050106 WO 2004-US6273 20040227 WO 2005001143 A3 20050506 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2005130174 A1 20050616 US 2004-789831 20040227 EP 1597399 A2 20051123 EP 2004-775821 20040227 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRAI US 2003-450268P P 20030227 WO 2004-US6273 W 20040227
AB Methods of quantifying individual mRNAs in global anal. of gene expression using nanoparticle conjugates with oligo-(dT) probes in microarray assays is described. The method avoids the problems assocd. with fluorescent labeling and target amplification. The mRNA population is hybridized to a microarray. Hybrids are then labeled by hybridization with a probe for the ***poly*** (***A***) tail of the mRNA. The probe is conjugated with gold nanoparticles and this is used as a nucleus for signal amplification, e.g. by silver staining. The method is at least as sensitive as the use of fluorescent dye-labeled probes and is colinear in signal intensity over a 1000-fold range in mRNA concns.

=> s array?/bi,ab 156423 ARRAY?/BI 145638 ARRAY?/AB
L4 156423 ARRAY?/BI,AB

=> s microarray?/bi,ab 44879 MICROARRAY?/BI 25533 MICROARRAY?/AB
L5 44879 MICROARRAY?/BI,AB

=> s l4 or l5
L6 191121 L4 OR L5

=> l2 and l6
L2 IS NOT A RECOGNIZED COMMAND
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=> s l2 and l6
L7 420 L2 AND L6

=> l1 and l7
L1 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s l1 and l7
L8 2 L1 AND L7

=> l7 not 2006/py
L7 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s l7 not 2006/py 1139121 2006/PY
L9 326 L7 NOT 2006/PY

=> s l9 not 2005/py 1364069 2005/PY
L10 255 L9 NOT 2005/PY

=> s l10 not 2004/py 1322140 2004/PY
L11 205 L10 NOT 2004/PY

=> s l11 not 2003/py 1261103 2003/PY
L12 164 L11 NOT 2003/PY

=> d his
(FILE 'HOME' ENTERED AT 16:22:08 ON 15 NOV 2006)
FILE 'CAPLUS' ENTERED AT 16:22:29 ON 15 NOV 2006
L1 479 S (HYBRIDI?(20A)NANOPARTICLE#)/BI,AB
L2 20113 S ((POLYA) OR (POLY(W)A) OR (POLY(W)ADENYL?))/BI,AB
L3 2 S L1 AND L2
L4 156423 S ARRAY?/BI,AB
L5 44879 S MICROARRAY?/BI,AB
L6 191121 S L4 OR L5
L7 420 S L2 AND L6
L8 2 S L1 AND L7
L9 326 S L7 NOT 2006/PY
L10 255 S L9 NOT 2005/PY
L11 205 S L10 NOT 2004/PY
L12 164 S L11 NOT 2003/PY

=> s l8 not l3
L13 0 L8 NOT L3

=> s sandwich?/bi,ab 59588 SANDWICH?/BI
54159 SANDWICH?/AB
L14 59588 SANDWICH?/BI,AB

=> s l12 and l14
L15 0 L12 AND L14

=> d his
(FILE 'HOME' ENTERED AT 16:22:08 ON 15 NOV 2006)
FILE 'CAPLUS' ENTERED AT 16:22:29 ON 15 NOV 2006
L1 479 S (HYBRIDI?(20A)NANOPARTICLE#)/BI,AB
L2 20113 S ((POLYA) OR (POLY(W)A) OR (POLY(W)ADENYL?))/BI,AB
L3 2 S L1 AND L2
L4 156423 S ARRAY?/BI,AB
L5 44879 S MICROARRAY?/BI,AB
L6 191121 S L4 OR L5
L7 420 S L2 AND L6
L8 2 S L1 AND L7
L9 326 S L7 NOT 2006/PY
L10 255 S L9 NOT 2005/PY
L11 205 S L10 NOT 2004/PY
L12 164 S L11 NOT 2003/PY
L13 0 S L8 NOT L3
L14 59588 S SANDWICH?/BI,AB
L15 0 S L12 AND L14

=> d l12 1-164 bib ab

L12 ANSWER 1 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:272883 CAPLUS <<LOGINID::20061115>>
DN 142:312643
TI Normalization of gene expression data with the ***ArrayFit*** system
AU Vonderstrass, S.; Hallensleben-Steen, W.
CS GeneScan Europe AG, Freiburg, 79108, Germany
SO Bioforum (2002), 25(4), 189-190 CODEN: BFRME3; ISSN: 0940-0079
PB G.I.T. Verlag Publishing Ltd.
DT Journal
LA German
AB The ***ArrayFit*** system is presented for the normalization of gene expression data using 5 polyadenylated RNAs to be analyzed together with the RNA samples.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:592713 CAPLUS <<LOGINID::20061115>>
DN 140:13489
TI Rapidly isolating total RNA from wheat
AU Gong, Ligui; Shen, Longzhu; Xu, Ziqin
CS Life Science School, Northwest University, Xian, Shanxi Province, 710069, Peop. Rep. China
SO Jiguang Shengwu Xuebao (2002), 11(4), 301-304 CODEN: JSXUFX; ISSN: 1007-7146
PB Jiguang Shengwu Xuebao Bianjibu
DT Journal
LA English
AB RNeasy Kits are used to isolate total RNA from small quantities of wheat. They provide a fast and simple method to make the multiple, simultaneous processing of a wide variety of biol. samples possible in less than 30 min. The use of toxic substance such as phenol and/or chloroform is replaced by the RNeasy procedure. The purified RNA is ready for the use in std. and downstream applications such as RT-PCR, ***polyA*** +RNA selection, differential display, Northern dot and slot blotting, primer extension, cDNA synthesis, expression ***array*** and expression-chip anal. We have successfully isolated total RNA from wheat with RNeasy Kit for many times, three of which were analyzed in this paper. The value of OD260 nm/OD280 nm was in the range from 1.7 to 1.9 and that of OD260 nm/OD230 nm was more than 2.0, which indicated that the purity of RNA was satisfactorily high and not contaminated by proteins or benzene phenol etc..
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:324418 CAPLUS <<LOGINID::20061115>>
DN 139:275545
TI Gene expression differential study in peripheral blood mononuclear cell (PBMC) of patients with SLE and IDDM
AU Wang, Jing; Qian, Dongmeng; Gao, Meihua; Li, Wenli; Wang, Bin
CS Department of Immunology, Qingdao University Medical College, Tsingtao, 266021, Peop. Rep. China
SO Zhongguo Mianyixue Zazhi (2002), 18(10), 720-723 CODEN: ZMZAEE; ISSN: 1000-484X
PB Zhongguo Mianyixue Zazhi Bianjibu
DT Journal
LA Chinese
AB The differential gene expression between systemic lupus erythematosus (SLE) and insulin-dependent diabetes mellitus (IDDM) with patients was studied. The cDNA probes were synthesized from ***polyA*** + RNA of PBMC in SLE and IDDM patients, and were differentially hybridized with two identical Atlas cDNA expression ***array*** membranes contg. 1176 known genes. Autoradiog. anal. showed that 376 genes were showed differential expression in SLE disease, 8 were found up- regulated, and 6 down-regulated (ratio > 6); the 558 genes were showed differential expression in IDDM disease, 13 were found up-regulated (ratio > 6), and 3 down-regulated (ratio

> 6). The genes, which were assocd. with the regulation of cell differentiation and proliferation, adhesion and signal transduction, apoptosis, transcription and modulation, and DNA damage and repair that, were changed obviously. The differential hybridization anal. of Atlas cDNA expression ***arrays*** can be a useful method for analyzing the expression profiles of PBMC genes and studying genes differential expression in SLE and IDDM patients.

L12 ANSWER 4 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:265569 CAPLUS <<LOGINID::20061115>>
DN 139:128722
TI Differential gene expression in sugarcane leaf and internodal tissues of varying maturity
AU Carson, D. L.; Huckett, B. I.; Botha, F. C.
CS Biotechnology Department, South African Sugar Association Experiment Station, Mount Edgecombe, 4300, S. Afr.
SO South African Journal of Botany (2002), 68(4), 434-442
CODEN: SAJBDD; ISSN: 0254-6299
PB NISC Pty Ltd.
DT Journal
LA English
AB The expression patterns of sugarcane (Saccharum spp. hybrids) genes were examd. in different tissue sources and at developmental stages by "reverse Northern" hybridization anal. to identify differentially expressed genes. CDNA ***arrays*** contg. 1 000 random clones from an immature leaf and maturing culm cDNA library were hybridized with radioactively-labeled ***poly*** (***A***)+ RNA from immature leaf, mature leaf, immature culm and maturing culm. All cDNAs were found to hybridize to all four probes, but differences in signal intensity were obsd. for individual cDNAs between hybridization events. No cDNAs displaying tissue- or developmental-stage specific expression were detected. Comparisons between hybridization patterns identified 61 cDNAs that were more abundantly expressed in immature and mature leaf than the culm. Likewise, 25 cDNAs preferentially expressed in immature and maturing culm were detected. ESTs established for the differentially expressed cDNAs revealed sequence homol. to a diverse collection of genes in both the leaf and the culm. These included genes assocd. with general cellular metab., transport, regulation and a variety of stress responses. None of the differentially expressed genes identified in the culm were homologous to genes known to be assocd. with sucrose accumulation. These preliminary gene expression profiling results suggest that the genetic regulation of processes related to sugarcane leaf and culm maturation is very complex.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:263696 CAPLUS <<LOGINID::20061115>>
DN 138:249540
TI EST sequencing, annotation and ***microarray*** transcriptome analysis identify preferentially root-expressed genes in sugar beet
AU Bellin, D.; Werber, M.; Theis, T.; Schulz, B.; Weisshaar, B.; Schneider, K.
CS Max-Planck-Institut fur Zuchtungsforschung, Koln, 50829, Germany
SO Plant Biology (Stuttgart, Germany) (2002), 4(6), 700-710
CODEN: PBIOFN; ISSN: 1435-8603
PB Georg Thieme Verlag
DT Journal
LA English
AB An integrated approach involving EST sequencing, data mining and multiparallel expression profiling by ***microarray*** anal. was established to classify sugar beet gene products with respect to their expression in three different organs. The DNA sequences of 2996 ESTs derived from young sugar beet plants specified 2048 unique gene products with putative functions in primary and secondary metab. (651), transport processes (136), signal transduction (78) and cellular organization (39). The cDNA clone collection was the basis for the generation of a ***microarray*** . Sensitivity and reproducibility of the ***microarray*** hybridization procedure were estd. first. The detection limit corresponded to 10-50 copies of single transcripts per cell. Within an interval of 2-fold variation in signal intensities, reproducibility between spots on the same filter was 98.9%, between spots on different filters 89.8%, and reproducibility after hybridization with two probes synthesized from the same ***poly*** (***A***)+ RNA sample was 97.6%. Expression profiles from roots, leaves, and inflorescences of field-grown plant material were generated. Two different samples of each organ were analyzed to reduce sampling effects, which accounted on av. for 30.3% of spots with at least 2-fold deviation. Expression values for each organ were detd. by a stringent statistical evaluation of 8 hybridizations for each clone. ***Microarray*** expression data were confirmed by Northern blot anal. and quant. RT-PCR expts. concerning 11 cDNAs. The anal. then focused on 76 unique cDNAs, for which the amt. of detected transcript in roots was at least twice as high as in the other organs tested. Functions of preferentially root-expressed candidate genes in taproot morphol. and physiol. are discussed. The EST sequences are deposited in GenBank/EMBL/DDBJ under accession nos. BQ487526-BQ490673 and BQ654408-BQ654412.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 6 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:175670 CAPLUS <<LOGINID::20061115>>
DN 138:363349
TI Outliers involving the ***poly*** (***A***) effect among highly-expressed genes in ***microarrays***
AU Pan, Shujia J.; Rigney, David R.; Ivy, John L.
CS Department of Kinesiology and Health Education, University of Texas at Austin, Austin, TX, 78712, USA
SO BMC Genomics [online computer file] (2002), 3, No pp. given CODEN: BGMEET; ISSN: 1471-2164 URL: http://www.biomedcentral.com/1471-2164/3/35
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB The ***Poly*** (***A***) effect is a cross-hybridization artifact in which poly(T)-contg. mols., which are produced by the reverse transcription of a ***poly*** (***A***)+ RNA mixt., bind promiscuously to the ***poly*** (***A***) stretches of the DNA in ***microarray*** spots. It is customary to attempt to block such hybridization by adding ***poly*** (***A***) to the hybridization soln. This note describes an expt. intended to evaluate circumstances under which the blocking procedure may not have been successful. The expt. involves a spot-by-spot comparison between the hybridization signals obtained by hybridizing a ***microarray*** to: (1) end-labeled oligo(dT), vs., (2) cDNA prepd. from muscle tissue. We found that the blocking appears to be successful for the vast majority of ***microarray*** spots, as evidenced by the weakness of the correlation between signals (1) and (2). However, we found that for

microarray spots having oligo(dT) hybridization levels greater than a certain threshold, the blocking might be ineffective or incomplete, as evidenced by an exceptionally strong signal (2) whenever signal (1) is greater than the threshold. In conclusion, the ***PolyA*** effect may be more subtle than simply a hybridization signal that is proportional to the ***PolyA*** content of each ***microarray*** spot. It may instead be present only in spots that hybridize oligo(dT) greater than some threshold level. The strong signal generated at these "outlier" spots by cDNA probes might be due to the formation of hybridization heteropolymers.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 7 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:161149 CAPLUS <<LOGINID::20061115>>
DN 138:379871
TI Isolation of genes that are induced by Ty21a in intestinal cells by suppression subtractive hybridization(SSH)
AU Wang, Hua; Gao, Jieying; Zhou, Jie; Li, Haimin
CS Laboratory of Immunology, Institute of Microbiology and Epidemiology, Academy of Military Medical Science, Beijing, 100071, Peop. Rep. China
SO Zhongguo Mianyixue Zazhi (2002), 18(8), 521-524 CODEN: ZMZAEE; ISSN: 1000-484X
PB Zhongguo Mianyixue Zazhi Bianjibu
DT Journal
LA Chinese
AB The genes induced by Ty21a were isolated. The intestinal cells of Balb/C mouse with and without Ty21a immunization prepd. and, the ***polyA*** + RNA was extd., the dscDNA was synthesized by using reverse transcription-PCR, the differentially expressed genes was got by suppression subtractive hybridization(SSH). Seven genes were novel genes revealed by GenBank searching whose expression were probably induced by Ty21a were isolated by SSH and cDNA ***microarray*** . The full length cDNA sequence of three genes are now obtaining through RACE-PCR. SSH is an effective method for isolating the differentially expressed genes; High throughput cDNA ***microarray*** is a credibility method to profile changes in gene expression; Ty21a can induce the expression of some new genes related to immune.

L12 ANSWER 8 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:15083 CAPLUS <<LOGINID::20061115>>
DN 138:249236
TI Optimization and evaluation of T7 based RNA linear amplification protocols for cDNA ***microarray*** analysis
AU Zhao, Hongjuan; Hastie, Trevor; Whitfield, Michael L.; Borresen-Dale, Anne-Lise; Jeffrey, Stefanie S.
CS Department of Surgery, Stanford University, Stanford, CA, 94305-5494, USA
SO BMC Genomics [online computer file] (2002), 3, No pp. given CODEN: BGMEET; ISSN: 1471-2164 URL: http://www.biomedcentral.com/1471-2164/3/31
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB T7-based linear amplification of RNA is used to obtain sufficient antisense RNA for ***microarray*** expression profiling. The fidelity and reproducibility of different amplification protocols were optimized and systematically evaluated using total RNA obtained from primary human breast carcinomas and high-d. cDNA ***microarrays*** . Using an optimized protocol, the av. correlation coeff. of gene expression of 11,123 cDNA clones between amplified and unamplified samples is 0.82 (0.85 when a virtual ***array*** was created using repeatedly amplified samples to minimize exptl. variation). Less than 4% of genes show changes in expression level by 2-fold or greater after amplification compared to unamplified samples. Most changes due to amplification are not systematic both within one tumor sample and between different tumors. Amplification appears to dampen the variation of gene expression for some genes when compared to unamplified ***poly*** (***A***)+ RNA. The reproducibility between repeatedly amplified samples is 0.97 when performed on the same day, but drops to 0.90 when performed weeks apart. The fidelity and reproducibility of amplification is not affected by decreasing the amt. of input total RNA in the 0.3-3 .mu.g range. Adding template-switching primer, DNA ligase, or column purifn. of double-stranded cDNA does not improve the fidelity of amplification. The correlation coeff. between amplified and unamplified samples is higher when total RNA is used as template for both exptl. and ref. RNA amplification. Thus, T7-based linear amplification reproducibly generates amplified RNA that closely approximates original sample for gene expression profiling using cDNA ***microarrays*** .
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 9 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:968688 CAPLUS <<LOGINID::20061115>>
DN 138:235976
TI Expression profiling of liver cell lines expressing entire or parts of hepatitis C virus open reading frame
AU Aizaki, Hideki; Harada, Takashi; Otsuka, Motoyuki; Seki, Naohiko; Matsuda, Mami; Li, Yue Wei; Kawakami, Hayato; Matsuura, Yoshiharu; Miyamura, Tatsuo; Suzuki, Tetsuro
CS Department of Virology II, National Institute of Infectious Diseases, Tokyo, Japan
SO Hepatology (Philadelphia, PA, United States) (2002), 36(6), 1431-1438 CODEN: HPTLD9; ISSN: 0270-9139
PB W. B. Saunders Co.
DT Journal
LA English
AB Although hepatitis C virus (HCV) is a causative agent of liver diseases, its mechanism of pathogenesis is still unclear, mainly because of the lack of adequate cell culture systems to support HCV infection and replication. In this report, we describe development and characterization of human hepatoma cell lines constitutively expressing entire (Hep394) or parts (Hep352, Hep3294) of the HCV open reading frame (ORF). The viral and cellular proteolytic machinery involved in the viral precursor processing was consistently functional, and processed HCV proteins were synthesized in these established cell lines. By using a cDNA ***microarray*** anal. coupled with semiquant. reverse-transcription polymerase chain reaction (RT-PCR), we identified 12 genes up-regulated and 4 genes down-regulated in Hep394 cells. With regard to genes related to cell growth regulation, we found up-regulation of forkhead transcription factor FREAC-1, ***poly*** (***A***) binding protein PABP2, and Ras suppressor Rsu-1. Another category of changes in gene expression includes MHC antigens, which play an important role in the T-cell-mediated immune reaction in the liver. In conclusion, functional genomic approaches comparing expression among the different cell lines expressing parts of the HCV genome may promote our understanding of the mol. basis of pathogenicity of HCV infection.

RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 10 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:954877 CAPLUS <<LOGINID::20061115>>
DN 138:215975
TI Application of L-cysteine derivative to DNA ***microarray***
AU Nakauchi, Gen; Inaki, Yoshiaki; Kitaoka, Shiho; Yokoyama, Chieko; Tanabe, Tadashi
CS Department of Material and Life Science, Graduate School of Engineering, Osaka University, Osaka, 565-0871, Japan
SO Nucleic Acids Research Supplement (2002), 2(Twenty-ninth Symposium on Nucleic Acids Chemistry), 257-258 CODEN: NARSCE
PB Oxford University Press
DT Journal
LA English
AB S-carboxymethyl-L-cysteine derivs. of nucleic acid bases were prepd. as DNA chip probe. These compds. in vitro have been found to form stable complex with oligo-DNA and RNA. This paper deals with prepg. new DNA chip using L-cysteine deriv. synthetic nucleotides as probe and immobilized it to quartz plate by photosensitive PVA. Then the chip exposed with FITC labeled target DNA was obsd. by confocal fluorescence microscope.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 11 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:939998 CAPLUS <<LOGINID::20061115>>
DN 138:281304
TI Protease activated receptor-1 is down regulated by levonorgestrel in endometrial stromal cells
AU Hague, S.; Oehler, M. K.; MacKenzie, I. Z.; Bicknell, R.; Rees, M. C. P.
CS Nuffield Department of Obstetrics and Gynaecology, Univ. Oxford, Oxford, OX3 9DU, UK
SO Angiogenesis (2002), 5(1-2), 93-98 CODEN: AGIOFT; ISSN: 0969-6970
PB Kluwer Academic Publishers
DT Journal
LA English
AB Progestogens are used clin. for contraception, to control excessive menstrual bleeding and to oppose estrogen in hormone replacement therapy. The use of intrauterine levonorgestrel (LNG) is however, assocd. with endometrial atrophy and decidualization of the stroma. In this study, the authors aimed to identify genes whose expression is modulated by LNG either alone or in combination with progesterone. Thus endometrial stromal cells were stimulated with progesterone, LNG or LNG and progesterone. ***Poly*** - ***A*** RNA was isolated and used to probe expression ***arrays*** . The expression of a no. of genes was altered on exposure to LNG or LNG and progesterone. Alteration of expression patterns was confirmed using semi-quant. RT-PCR and western blot anal. In particular, the protease activated receptor-1 (PAR-1) gene that encodes a receptor for thrombin was down regulated. This is the first demonstration that PAR-1 is down regulated by the progestogen LNG in human endometrium. Alteration in the expression levels of this receptor may affect both growth and hemostatic activity within the endometrium and may account for the obsd. morphol. effects seen in users of intrauterine LNG delivery devices.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 12 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:937303 CAPLUS <<LOGINID::20061115>>
DN 138:20443
TI Endocrine disruptor screening using DNA chips of endocrine disruptor-responsive genes
IN Kondo, Akihiro; Takeda, Takeshi; Mizutani, Shigetoshi; Tsujimoto, Yoshimasa; Takashima, Ryokichi; Enoki, Yuki; Kato, Ikunoshin
PA Takara Bio Inc., Japan
SO Jpn. Kokai Tokkyo Koho, 386 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2002355079 A2 20021210 JP 2002-69354 20020313
PRAI JP 2001-73183 A 20010314 JP 2001-74993 A 20010315 JP 2001-102519 A 20010330
AB A method and kit for detecting endocrine-disrupting chems. using DNA ***microarrays*** are claimed. The method comprises prepg. a nucleic acid sample contg. mRNAs or cDNAs originating in cells, tissues, or organisms which have been brought into contact with a sample contg. the endocrine disruptor. The nucleic acid sample is hybridized with DNA ***microarrays*** having genes affected by the endocrine disruptor or DNA fragments originating in these genes have been fixed. The results obtained are then compared with the results obtained with the control sample to select the gene affected by the endocrine disruptor. Genes whose expression is altered by tri-Bu tin, 4-octaphenol, 4-nonylphenol, di-N-Bu phthalate, dichlorohexyl phthalate, octachlorostyrene, benzophenone, diethylhexyl phthalate, diethylstilbestrol (DES), and 17-.beta. estradiol (E2), were found in mice by DNA chip anal.

L12 ANSWER 13 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:924552 CAPLUS <<LOGINID::20061115>>
DN 138:34129
TI Protein and cDNA sequences of human ***poly*** (***A***)-binding protein 33.11 and therapeutical uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 35 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1340520 A 20020320 CN 2000-119821 20000831
PRAI CN 2000-119821 20000831
AB The invention provides the protein and cDNA sequences of a novel human ***poly*** (***A***)-binding protein 33.11 with the mol. wt. of 33 kilodaltons cloned from human fetal brain. In particular, the invention discloses that the gene encoding this protein has a similar gene expression pattern with gene encoding

poly (***A***)-binding protein. The invention also relates to construction of ***poly*** (***A***)-binding protein 33.11 expression vector for prepn. of recombinant protein using prokaryotes or eukaryotes. The invention relates to prepn. of antibody against this protein. The invention further relates to the PCR primers, nucleic acid probes, DNA fragments and protein agonists or antagonists specific for this gene or gene product for the diagnosis as well as treatment of various diseases, such as embryonic development malformation, protein metab. disorder, neoplasm, etc.

L12 ANSWER 14 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:921851 CAPLUS <<LOGINID::20061115>>
DN 137:364371
TI Methods and kits for gene expression profiling for cancer diagnosis using ***arrays***
IN Chenchik, Alex; Siebert, Paul; Herrler, Michael
PA Clontech Laboratories, Inc., USA
SO U.S., 16 pp., Cont.-in-part of U.S. 6,287,768. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 6489159 B1 20021203 US 2000-675915 20000929 US 6087102 A 20000711 US 1998-3723 19980107 WO 9935289 A1 19990715 WO 1999-US248 19990106 W: AU, CA, JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US 6287768 B1 20010911 US 2000-269586 20000303
PRAI US 1998-3723 A2 19980107 WO 1999-US248 W 19990106 US 2000-269586 A2 20000303
AB ***Arrays*** of a plurality of different heterogeneous polymeric target compns. immobilized on the surface of a solid support are provided. In the subject ***arrays*** , the constituent polymeric targets of the heterogeneous target compns. are generally biopolymeric compds., e.g., nucleic acids and proteins, where ribonucleic acids and proteins are the preferred polymeric targets in many embodiments. The subject ***arrays*** find use in a variety of different applications, including high throughput gene expression anal. of tumors for cancer diagnosis.
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 15 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:861822 CAPLUS <<LOGINID::20061115>>
DN 138:52439
TI Maculavirus, a new genus of plant viruses
AU Martelli, G. P.; Sabanadzovic, S.; Ghanem-Sabanadzovic, N. Abou; Saldarelli, P.
CS Dipartimento di Protezione delle Piante e Microbiologia Applicata, Universita degli Studi and Istituto di Virologia Vegetale del CNR, Sezione di Bari, Italy
SO Archives of Virology (2002), 147(9), 1847-1853 CODEN: ARVIDF; ISSN: 0304-8608
PB Springer-Verlag Wien
DT Journal; General Review
LA English
AB A review. Maculavirus is a new genus of plant viruses typified by Grapevine fleck virus (GFkV). A possible second member is Grapevine redglobe virus (GRGV). Maculaviruses are phloem-limited non-mech. transmissible viruses with isometric particles c. 30 nm in diam. that have a rounded contour and prominent surface structure. Vectors, if any, are unknown. GFkV prepns. contain two centrifugal components, T made up of empty protein shells and B, which contains 35% RNA. The coat protein (CP) has a mol. mass of 24 kDa. The genome is a single-stranded RNA that has c. 50% cytosine residues. It is 7564 nt in size, excluding the ***poly*** (***A***) tail and contains four putative open reading frames (ORF) that encode a 215.4 kDa polypeptide with the conserved motifs of replication-assocd. proteins of pos.-strand RNA viruses (ORF1), the CP (ORF2), and one (GRGV) or two (GFkV) proline-rich polyproteins of 31.4 kDa (ORF3) and 15.9 kDa (ORF4), resp., with unknown function. Replication-assocd. proteins and CP are phylogenetically related to those of members of the genera Tymovirus and Marafivirus. GFkV-infected grapevine cells contain vesiculated mitochondria, the possible site of RNA replication. In the natural host, GFkV particles accumulate in great quantity, sometimes in cryst. ***arrays*** in phloem cells.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 16 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:832556 CAPLUS <<LOGINID::20061115>>
DN 137:350862
TI Gene expression profiles in bone and cartilage formation and their use in diagnosis and treatment of disease
IN Clancy, Brian; Pittman, Debra M.
PA Wyeth, John, and Brother Ltd., USA
SO PCT Int. Appl., 197 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2002085285 A2 20021031 WO 2002-US12149 20020418 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-284786P P 20010418
AB The invention provides methods and compns. for diagnostic assays for detecting bone and cartilage formation and therapeutic methods and compns. for treating disease and disorders related to bone and cartilage formation or resorption, such as osteoporosis and bone fractions. The invention also provides therapeutic methods for diseases related to bone or cartilage formation or resorption. Methods for identifying therapeutics for such diseases are also provided. Marker genes that can be used to monitor bone and cartilage formation are identified on com.
DNA ***microarrays*** .

L12 ANSWER 17 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:805584 CAPLUS <<LOGINID::20061115>>
DN 138:314079

TI Common gene targets of Ginkgo biloba extract (EGb 761) in human tumor cells: Relation to cell growth
AU Li, Wenping; Pretner, Ewald; Shen, Liya; Drieu, Katy; Papadopoulos, Vassilios
CS Division of Hormone Research, Dept. of Cell Biology, Pharmacology and Neurosciences, Georgetown University Medical Center, Washington, DC, 20057, USA
SO Cellular and Molecular Biology (Paris, France, Printed) (2002), 48(6), 655-662 CODEN: CMOBEF; ISSN: 0145-5680
PB CMB Association
DT Journal
LA English
AB The standardized ext. of Ginkgo biloba leaves (EGb 761) has been shown to inhibit aggressive human breast cancer cell proliferation both in vitro and in vivo. These results were extended to human glioma and hepatoma cells in vitro suggesting that EGb 761 may have a more widespread application for tumor growth control. To understand the mechanism by which EGb 761 acts to inhibit cell proliferation, we investigated the effects of EGb 761 on human breast cancer, glioma and hepatoma cell transcriptomes by means of various large-scale DNA ***array*** techniques. The data presented focus on genes regulated by EGb 761 that are common to the three tumor cell types and for which the data were verified by two different types of DNA ***microarray*** and/or RNA (Northern) blot anal. and real-time quant. PCR. These results could therefore help elucidate the mechanism of cytostatic action of EGb 761 and identify genes important for tumor growth.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 18 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:777950 CAPLUS <<LOGINID::20061115>>
DN 137:273158
TI Methods for diagnosing and treating multiple sclerosis and compositions thereof
IN Trepicchio, William L.; Oestreicher, Judith L.; Leonard, John P.; Dorner, Andrew J.; Hunter, Sharon E.
PA Wyeth, John, and Brother Ltd., USA
SO PCT Int. Appl., 178 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2002079218 A1 20021010 WO 2002-US9305 20020327 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-280572P P 20010330
AB The present invention is directed to novel methods for diagnosis and prognosis of Multiple Sclerosis by identifying differentially expressed genes. Moreover, the present invention is also directed to methods that can be used to screen test compds. and therapies for the ability to inhibit multiple sclerosis. Addnl., methods and mol. targets (genes and their products) for therapeutic intervention in multiple sclerosis are described.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 19 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:772513 CAPLUS <<LOGINID::20061115>>
DN 138:118255
TI Expression profiling of Drosophila imaginal discs
AU Klebes, Ansgar; Biehs, Brian; Cifuentes, Francisco; Kornberg, Thomas B.
CS Department of Biochemistry and Biophysics, University of California, San Francisco, CA, 94143, USA
SO GenomeBiology [online computer file] (2002), 3(8), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/content/pdf/gb-2002-3-8-research0038.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: In the Drosophila larva, imaginal disks are programmed to produce adult structures at metamorphosis. Although their fate is precisely detd., these organs remain largely undifferentiated in the larva. To identify genes that establish and express the different states of detn. in disks and larval tissues, we used DNA ***microarrays*** to analyze mRNAs isolated from single imaginal disks. Results: Linear amplification protocols were used to generate hybridization probes for ***microarray*** anal. from ***poly*** (***A***)+ RNA from single imaginal disks contg. between 10,000 and 60,000 cells. Probe reproducibility and degree of representation were tested using ***microarrays*** with approx. 6,000 different cDNAs. Hybridizations with probes that had been prepd. sep. from the same starting RNA pool had a correlation coeff. of 0.97. Expression profile comparisons of the left and right wing imaginal disks from the same larva correlated with a coeff. of 0.99, indicating a high degree of reproducibility of independent amplifications. Using this method, we identified genes with preferential expression in the different imaginal disks using pairwise comparisons of disks and larval organs. Whereas disk-to-disk comparisons revealed only moderate differences, profiles differed substantially between imaginal disks and larval tissues, such as larval endodermal midgut and mesodermal fat body. Conclusion: The combination of linear RNA amplification and DNA ***microarray*** hybridization allowed us to det. the expression profiles of individual imaginal disks and larval tissues and to identify genes expressed in tissue-specific patterns. These methods should be widely applicable to comparisons of expression profiles for tissues or parts of tissues that are available only in small amts.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 20 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:754629 CAPLUS <<LOGINID::20061115>>
DN 137:274030
TI Methods for designing and identifying nucleic acid molecules of interest as "representative gene fragments" for use in hybridization ***arrays***
IN Simpson, Andrew J. G.; De Souza, Sandro J.; Brentani, Ricardo R.
PA Ludwig Institute for Cancer Research, USA

SO PCT Int. Appl., 23 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2002077288 A1 20021003 WO 2002-US8705 20020321 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-278485P P 20010323 US 2001-300998P P 20010626
AB The invention relates to methods for improving the ability to obtain mols. which are useful in oligonucleotide screening assays. By assaying a library for appropriate mols. using a set of defined parameters, one can identify a set of mols. which will facilitate oligonucleotide hybridization assays more efficiently. These so called "representative gene fragments" (RGSs) mols. are designed with the use of computer software to screen databases to det. nucleotide sequences for use as target mols. on a given surface, such as a biochip. The criteria used in the design include: (i) defined length; (ii) defined GC content; (iii) defined position of a sequence in a cDNA mol. relative to the ***poly*** (***A***) tail of a cDNA mol.; (iv) level of expression based upon size of a UniGene cluster; (v) absence of repetitive elements; (vi) differences in overall sequence from any other sequences in the same organism based upon a min. threshold value of, e.g., 75 % , and; (vii) presence of a synthetic sequence, i.e., a sequence defined by two or more fragments of a cDNA mol. which are not contiguous in the available mols. The RGSs further identified from ***microarray*** have the capacity to faithfully reflect gene expressed levels and avoid cross hybridization between members of the same gene family. The invention provides for solid phase ***arrays*** of mols. which can, in turn, be used in further ***microarray*** anal. In particular, a library of probes has been developed to analyze a cDNA library from a colon cancer line to det. gene expression frequency. No cross hybridization between members of the same family are demonstrated in the family for human solute carrier 12 and cadherin 12.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 21 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:749784 CAPLUS <<LOGINID::20061115>>
DN 137:261835
TI Epstein-Barr virus-induced changes in B-lymphocyte gene expression
AU Carter, Kara L.; Cahir-McFarland, Ellen; Kieff, Elliott
CS Departments of Medicine and Microbiology and Molecular Genetics, Harvard Medical School, Brigham and Women's Hospital, Boston, MA, 02115, USA
SO Journal of Virology (2002), 76(20), 10427-10436 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB To elucidate the mechanisms by which Epstein-Barr virus (EBV) latency III gene expression transforms primary B lymphocytes to lymphoblastoid cell lines (LCLs), the assocd. alterations in cell gene expression were assessed by using 4,146 cellular cDNAs ***arrayed*** on nitrocellulose filters and real-time reverse transcription-PCR (RT-PCR). A total of 1,405 of the 4,146 cDNAs were detected using cDNA probes from ***poly*** (***A***)+ RNA of IB4 LCLs, a non-EBV-infected Burkitt's lymphoma (BL) cell line, BL41, or EBV latency III-converted BL41 cells (BL41EBV). Thirty-eight RNAs were consistently twofold more abundant in the IB4 LCL and BL41EBV than in BL41 by ***microarray*** anal. Ten of these are known to be EBV induced. A total of 23 of 28 newly identified EBV-induced genes were confirmed by real-time RT-PCR. In addn., nine newly identified genes and CD10 were EBV repressed. These EBV-regulated genes encode proteins involved in signal transduction, transcription, protein biosynthesis and degrdn., and cell motility, shape, or adhesion. Seven of seven newly identified EBV-induced RNAs were more abundant in newly established LCLs than in resting B lymphocytes. Surveys of eight promoters of newly identified genes implicate NF-.kappa.B or PU.1 as potentially important mediators of EBV-induced effects through LMP1 or EBNA2, resp. Thus, examn. of the transcriptional effects of EBV infection can elucidate the mol. mechanisms by which EBV latency III alters B lymphocytes.
RE.CNT 126 THERE ARE 126 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 22 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:715599 CAPLUS <<LOGINID::20061115>>
DN 138:729
TI Differential display technology: a general guide
AU Stein, J.; Liang, P.
CS Department of Zoology, University of British Columbia, Vancouver, BC, V7T 1Z4, Can.
SO Cellular and Molecular Life Sciences (2002), 59(8), 1235-1240 CODEN: CMLSFI; ISSN: 1420-682X
PB Birkhaeuser Verlag
DT Journal; General Review
LA English
AB A review. This article reviews the development of the differential display (DD) technol. and certain problems assocd. with DD. The authors also address issues related to other differential gene expression anal. techniques and discuss how these techniques can be used to complement DD.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 23 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:651751 CAPLUS <<LOGINID::20061115>>
DN 137:347097
TI Chromosomal clustering of muscle-expressed genes in Caenorhabditis elegans
AU Roy, Peter J.; Stuart, Joshua M.; Lund, Jim; Kim, Stuart K.
CS Departments of Developmental Biology and Genetics, Stanford University Medical Center, Stanford, CA, 94305, USA
SO Nature (London, United Kingdom) (2002), 418(6901), 975-979 CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English

AB Chromosomes are divided into domains of open chromatin, where genes have the potential to be expressed, and domains of closed chromatin, where genes are not expressed. Classic examples of open chromatin domains include puffs' on polytene chromosomes in Drosophila and extended loops from lampbrush chromosomes. If multiple genes were typically expressed together from a single open chromatin domain, the position of co-expressed genes along the chromosomes would appear clustered. To investigate whether co-expressed genes are clustered, we examd. the chromosomal positions of the genes expressed in muscle of Caenorhabditis elegans at the first larval stage. Here we show that co-expressed genes in C. elegans are clustered in groups of 2-5 along the chromosomes, suggesting that expression from a chromatin domain can extend over several genes. These observations reveal a higher-order organization of the structure of the genome, in which the order of genes along the chromosome is correlated with their expression in specific tissues.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 24 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:497797 CAPLUS <<LOGINID::20061115>>
DN 137:258260
TI DNA ***array*** profiling of gene expression changes during maize embryo development
AU Lee, Jian-Ming; Williams, Mark E.; Tingey, Scott V.; Rafalski, J. Antoni
CS DuPont Crop Genetics, Newark, DE, 19714, USA
SO Functional & Integrative Genomics (2002), 2(1-2), 13-27 CODEN: FIGUBY; ISSN: 1438-793X
PB Springer-Verlag
DT Journal
LA English
AB DNA ***microarray*** -based gene expression profiling was used to classify temporal patterns of gene expression during the development of maize embryos, to understand mRNA-level control of embryogenesis and to dissect metabolic pathways and their interactions in the maize embryo. Genes involved in carbohydrate, fatty acid, and amino acid metab., the tricarboxylic acid (TCA) cycle, glycolysis, the pentose phosphate pathway, embryogenesis, membrane transport, signal transduction, cofactor biosynthesis, photosynthesis, oxidative phosphorylation and electron transfer, as well as 600 random complementary DNA (cDNA) clones from maize embryos, were ***arrayed*** on glass slides. DNA ***arrays*** were hybridized with fluorescent dye-labeled cDNA probes synthesized from kernel and embryo ***poly*** (***A***)+RNA from different stages of maize seed development. Several characteristic developmental patterns of expression were identified and correlated with gene function. Patterns of coordinated gene expression in the TCA cycle and glycolysis were analyzed in detail. The steady state level of ***poly*** (***A***)+ RNA for many genes varies dramatically during maize embryo development. Expression patterns of genes coding for enzymes of fatty acid biosynthesis and glycolysis are coordinately regulated during development. Genes of unknown function may by assigned a hypothetical role based on their patterns of expression resembling well characterized genes. Electronic supplementary material to this paper can be obtained by using the Springer LINK server located at http://dx.doi.org/10.1007/s10142-002-0046-6.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 25 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:485604 CAPLUS <<LOGINID::20061115>>
DN 137:273640
TI Amine-modified random primers to label probes for DNA ***microarrays***
AU Xiang, Charlie C.; Kozhich, Olga A.; Chen, Mei; Inman, Jason M.; Phan, Quang N.; Chen, Yidong; Brownstein, Michael J.
CS Laboratory of Genetics, National Institute of Mental Health, Bethesda, MD, 20892, USA
SO Nature Biotechnology (2002), 20(7), 738-742 CODEN: NABIF9; ISSN: 1087-0156
PB Nature Publishing Group
DT Journal
LA English
AB DNA ***microarrays*** have been used to study the expression of thousands of genes at the same time in a variety of cells and tissues. The methods most commonly used to label probes for ***microarray*** studies require a min. of 20 .mu.g of total RNA or 2 .mu.g of ***poly*** (***A***) RNA. This has made it difficult to study small and rare tissue samples. RNA amplification techniques and improved labeling methods have recently been described. These new procedures and reagents allow the use of less input RNA, but they are relatively time-consuming and expensive. Here we introduce a technique for prepg. fluorescent probes that can be used to label as little as 1 .mu.g of total RNA. The method is based on priming cDNA synthesis with random hexamer oligonucleotides, on the 5' ends of which are bases with free amino groups. These amine-modified primers are incorporated into the cDNA along with aminoallyl nucleotides, and fluorescent dyes are then chem. added to the free amines. The method is simple to execute, and amine-reactive dyes are considerably less expensive than dye-labeled bases or dendrimers.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 26 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:469213 CAPLUS <<LOGINID::20061115>>
DN 137:227141
TI A highly reproducible, linear, and automated sample preparation method for DNA ***microarrays***
AU Dorris, David R.; Ramakrishnan, Ramesh; Trakas, Dionisios; Dudzik, Frank; Belval, Richard; Zhao, Connie; Nguyen, Allen; Domanus, Marc; Mazumder, Abhijit
CS Motorola Life Sciences, Northbrook, IL, 60062, USA
SO Genome Research (2002), 12(6), 976-984 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB DNA ***microarrays*** are powerful tools to detect changes in transcript abundance in multiple samples in parallel. However, detection of differential transcript levels requires a reproducible sample (target) prepn. method in addn. to a high-performance ***microarray*** . Therefore, we optimized a target-prepn. method that converts the ***poly*** (***A***)+ RNA fraction of total RNA into complementary DNA, then generates biotin-labeled complementary RNA from the cDNA. We measured the efficiency of incorporation of biotin-contg.

nucleotides by an enzymic digestion, followed by resoln. via anal. high-performance liq. chromatog. (HPLC). When the target was hybridized to a sensitive and reproducible ***microarray*** platform, low coeffs. of variation in both hybridization intensities and differential expression ratios across target prepns. were obsd. Nearly identical hybridization intensities and expression ratios are obsd. regardless of whether ***poly*** (***A***)+-enriched RNA or total RNA is used as the starting material. We show the ability to discern biol. and prodn. variability through the use of different lots of com. samples as visualized by hierarchical clustering. Automation of the target-prepn. procedure shows equivalence to the manual procedure, reproducible yields of target, and low variability as measured by hybridization to ***microarrays*** . Most importantly, RNA mixing expts. show a linear and quant. amplification in probe hybridization signals for >6000 genes across the entire signal range.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 27 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:396058 CAPLUS <<LOGINID::20061115>>
DN 137:182732
TI Global gene profiling in human endometrium during the window of implantation
AU Kao, L. C.; Tulac, S.; Lobo, S.; Imani, B.; Yang, J. P.; Germeyer, A.; Osteen, K.; Taylor, R. N.; Lessey, B. A.; Giudice, L. C.
CS Department of Gynecology and Obstetrics, Stanford University, Stanford, CA, 94305, USA
SO Endocrinology (2002), 143(6), 2119-2138 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB Implantation in humans is a complex process that is temporally and spatially restricted. Over the past decade, using a one-by-one approach, several genes and gene products that may participate in this process have been identified in secretory phase endometrium. Herein, we have investigated global gene expression during the window of implantation (peak E2 and progesterone levels) in well characterized human endometrial biopsies timed to the LH surge, compared with the late proliferative phase (peak E2 level) of the menstrual cycle. Tissues were processed for ***poly*** (***A*** +) RNA and hybridization of chem. fragmented, biotinylated cRNAs on high d. oligonucleotide ***microarrays*** , screening for 12,686 genes and expressed sequence tags. After data normalization, mean values were obtained for gene readouts and fold ratios were derived comparing genes up- and down-regulated in the window of implantation vs. the late proliferative phase. Nonparametric testing revealed 156 significantly ($P < 0.05$) up-regulated genes and 377 significantly down-regulated genes in the implantation window. Up-regulated genes included those for cholesterol trafficking and transport [apolipoprotein (Apo)E being the most induced gene, 100-fold], prostaglandin (PG) biosynthesis (PLA2) and action (PGE2 receptor), proteoglycan synthesis (glucuronyltransferase), secretory proteins [glycodelin, mammaglobin, Dickkopf-1 (Dkk-1, a Wnt inhibitor)], IGF binding protein (IGFBP), and TGF-.beta. superfamilies, signal transduction, extracellular matrix components (osteopontin, laminin), neurotransmitter synthesis (monoamine oxidase) and receptors (.gamma. aminobutyric acid A receptor .pi. subunit), numerous immune modulators, detoxification genes (metallothioneins), and genes involved in water and ion transport [e.g. Clostridia Perfringens Enterotoxin (CPE) 1 receptor (CPE1-R) and K+ ion channel], among others. Down-regulated genes included intestinal trefoil factor (ITF) [the most repressed gene (50-fold)], matrilysin, members of the G protein-coupled receptor signaling pathway, frizzled-related protein (FrpHE, a Wnt antagonist), transcription factors, TGF-.beta. signaling pathway members, immune modulators (major histocompatibility complex class II subunits), and other cellular functions. Validation of select genes was conducted by Northern anal. and RT-PCR using RNA from endometrial biopsies obtained in the proliferative phase and the implantation window and by RT-PCR using RNA from cultured endometrial epithelial and stromal cells. These approaches confirmed up-regulation of genes corresponding to IGFBP-1, glycodelin, CPE1-R, Dkk-1, mammaglobin, and ApoD and down-regulation for PR membrane component 1, FrpHE, matrilysin, and ITF, as with the ***microarray*** data. Cultured endometrial epithelial cells were found to express mRNAs for glycodelin, CPE-1R, Dkk-1, the .gamma. aminobutyric acid A receptor .pi. subunit, mammaglobin, matrilysin, ITF and PR membrane component 1. The expression of IGFBP-1, CPE1-R, Dkk-1, and ApoD mRNAs increased upon decidualization of stromal cells in vitro with progesterone after E2 priming, whereas FrpHE decreased, consistent with the ***microarray*** results. Overall, the data demonstrate numerous genes and gene families not heretofore recognized in human endometrium or assocd. with the implantation process. Reassuringly, several gene products, known to be differentially expressed in the implantation window or in secretory endometrium, were verified, and the striking regulation of select secretory proteins, water and ion channels, signaling mols., and immune modulators underscores the important roles of these systems in endometrial development and endometrial-embryonic interactions. In addn., the current study validates using high d. oligonucleotide ***microarray*** technol. to investigate global changes in gene expression in human endometrium.
RE.CNT 80 THERE ARE 80 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 28 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:271076 CAPLUS <<LOGINID::20061115>>
DN 136:274286
TI DNA construct containing RNA polymerase I-specific rRNA gene promoter, IRES element and ***poly*** (***A***) signal, and its use in recombinant production of proteins in transfected cells
IN Palmer, Theodore D.; McStay, Brian M.; Miller, A. Dusty; Reeder, Ronald H.
PA Fred Hutchinson Cancer Research Center, USA
SO U.S., 22 pp., Cont.-in-part of U.S. Ser. No. 743,513, abandoned. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 6368862 B1 20020409 US 1992-845937 19920304
PRAI US 1991-743513 B2 19910812
AB The invention provides DNA constructs contg. four elements in a serial ***array*** which include nucleotide sequences for: (a) a RNA polymerase I-specific promoter from an eukaryotic (such as human or mouse) RNA gene; (b) an internal ribosome entry signal (IRES) element (from encephalomyocarditis virus);

(c) a protein of interest; and (d) a ***poly*** (***A***) signal (from SV40). The invention relates that the IRES element encodes a RNA which binds with the translation initiation complex and allows the protein of interest to be translated. The invention also provides the use of said constructs in prodn. of plasmids or genetic vectors for recombinant prodn. of said protein of interest in transformed cells. The invention also relates that the Pol I-specific expression level of the protein of interest is equal or higher than the Pol II-specific expression level. In the examples section, the invention presented the construction of various plasmids, including pHENA and pMENA which contain Pol I-specific rDNA promoters from human and mouse, resp., and use of said plasmids in recombinant prodn. of bacterial neomycin phosphotransferase in transfected cells.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 29 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:250454 CAPLUS <<LOGINID::20061115>>
DN 137:120237
TI Normalization of cDNA ***microarray*** data using exogenous nucleic acid control in gene differential expression determination
AU Zhang, Liang; Zhang, Jian; Zhou, Yu-xiang; Cheng, Jing
CS Department of Biological Science and Technology, Tsinghua University, Beijing, 100084, Peop. Rep. China
SO Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (2002), 18(1), 115-119 CODEN: ZSHXF2; ISSN: 1007-7626
PB Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao Bianweihui
DT Journal
LA Chinese
AB In DNA ***microarray*** technol., it is necessary to det. the detection sensitivity level and normalize the difference in Dye incorporation and quantum yield. In the past, the housekeeping genes were frequently used to normalize the ***microarray*** data. However, more recent reports indicate that the expression levels of housekeeping genes can vary. Three exogenous polyadenylated RNA were produced through in vitro transcription and used as internal control RNA, standing for high, medium and low abundance resp. The result showed that the fluorescent signal intensity of hybridization was pos. correlative with the gene transcript abundance and gene differential expression was identified in both DNA ***microarray*** and Northern blot methods.

L12 ANSWER 30 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:245875 CAPLUS <<LOGINID::20061115>>
DN 137:167154
TI Differential expression between pilocytic and anaplastic astrocytomas: identification of apolipoprotein D as a marker for low-grade, non-infiltrating primary CNS neoplasms
AU Hunter, Stephen; Young, Andrew; Olson, Jeffrey; Brat, Daniel J.; Bowers, Geoffrey; Wilcox, Josiah N.; Jaye, David; Mendrinos, Savvas; Neish, Andrew
CS Departments of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta, GA, 30322, USA
SO Journal of Neuropathology and Experimental Neurology (2002), 61(3), 275-281 CODEN: JNENAD; ISSN: 0022-3069
PB American Association of Neuropathologists, Inc.
DT Journal
LA English
AB Fibrillary astrocytoma, the most common primary central nervous system neoplasm, is infiltrating, rapidly proliferating, and almost invariably fatal. This contrasts with the biol. distinct pilocytic astrocytoma, which is circumscribed, often cystic, slowly proliferating, and assocd. with a favorable long-term outcome. Diagnostic markers for distinguishing pilocytic astrocytomas from infiltrating anaplastic astrocytomas are currently not available. To identify genes that might either serve as markers or explain these distinct biol. behaviors, cDNA ***microarray*** anal. was used to compare the expression of 7,073 genes (nearly one quarter of the human genome) between these 2 types of astrocytoma. MRNAs pooled from 3 pilocytic astrocytomas and from 4 infiltrating anaplastic astrocytomas were compared. Apolipoprotein D (apoD), which expressed 8.5-fold higher in pilocytic astrocytomas, showed the greatest level of differential expression and emerged as a potential marker for pilocytic tumors. By immunohistochem., 10 of 13 pilocytic astrocytomas stained pos. for apoD, while none of 21 infiltrating astrocytomas showed similar staining. ApoD immunostaining was also seen in 9 of 14 of gangliogliomas, 4 of 5 subependymal giant cell astrocytomas (SEGAs), and a single pleomorphic xanthoastrocytomas (PXAs). By in situ hybridization, pilocytic astrocytomas, in contrast with infiltrating astrocytomas, showed widespread increased apoD expression. SAGE anal. using the NCBI database showed a higher level of expression of apoD RNA in pilocytic astrocytoma than in any of the other 94 neoplastic and non-neoplastic tissues in the database. ApoD is assocd. with decreased proliferation in some cell lines, and is the protein found in highest concn. in cyst fluid from benign cystic disease of the breast. ApoD might play a role in either decreased proliferation or cyst formation in pilocytic astrocytomas, gangliogliomas, SEGAs, and PXAs.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 31 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:237472 CAPLUS <<LOGINID::20061115>>
DN 136:242730
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
SO Plant Physiology (2002), 128(3), 896-910 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
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L12 ANSWER 32 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:237470 CAPLUS <<LOGINID::20061115>>
DN 136:242729
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
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AN 2002:237467 CAPLUS <<LOGINID::20061115>>
DN 136:242728
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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DN 136:242727
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AN 2002:237463 CAPLUS <<LOGINID::20061115>>
DN 136:242726
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
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AN 2002:237456 CAPLUS <<LOGINID::20061115>>
DN 136:242725
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
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AN 2002:237454 CAPLUS <<LOGINID::20061115>>
DN 136:242724
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AN 2002:237451 CAPLUS <<LOGINID::20061115>>
DN 136:242723
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AN 2002:237448 CAPLUS <<LOGINID::20061115>>

DN 136:242721
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AN 2002:236671 CAPLUS <<LOGINID::20061115>>
DN 136:242720
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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DN 136:242719
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
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DT Journal
LA English
AB Assembly of 73,000 expressed sequence tags (ESTs) representing multiple organs and developmental stages of maize (Zea mays) identified .apprx.22,000 tentative unique genes (TUGs) at the criterion of 95% identity. Based on sequence similarity, overlap between any two of 9 libraries with >3000 ESTs ranged from 4 to 20% of the constituent TUGs. The most abundant ESTs were recovered from only one or a minority of the libraries, and only 26 EST contigs had members from all nine EST sets (presumably representing ubiquitously expressed genes). For several examples, ESTs for different members of gene families were detected in distinct organs. To study this further, 2 types of ***microarray*** slides were fabricated, one contg. 5534 ESTs from 10-14-day-old endosperm, and the other 4844 ESTs from immature ear, estd. to represent about 2800 and 2500 unique genes, resp. Each ***array*** type was hybridized with fluorescent cDNA targets prepd. from endosperm and immature ear ***poly*** (***A***)+ RNA. Although the 10-14-day-old postpollination endosperm TUGs showed only 12% overlap with immature ear TUGs, endosperm target hybridized with 94% of the ear TUGs, and ear target hybridized with 57% of the endosperm TUGs. Incomplete EST sampling of low-abundance transcripts contributes to an underest. of shared gene expression profiles. Reassembly of ESTs at the criterion of 90% identity suggests how cross hybridization among gene family members can overest. the overlap in genes expressed in ***microarray*** hybridization expts. [This abstr. record is one of fifteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 44 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:236665 CAPLUS <<LOGINID::20061115>>
DN 136:242717
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
SO Plant Physiology (2002), 128(3), 896-910 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Assembly of 73,000 expressed sequence tags (ESTs) representing multiple organs and developmental stages of maize (Zea mays) identified .apprx.22,000 tentative unique genes (TUGs) at the criterion of 95% identity. Based on sequence similarity, overlap between any two of 9 libraries with >3000 ESTs ranged from 4 to 20% of the constituent TUGs. The most abundant ESTs were recovered from only one or a minority of the libraries, and only 26 EST contigs had members from all nine EST sets (presumably representing ubiquitously expressed genes). For several examples, ESTs for different members of gene families were detected in distinct organs. To study this further, 2 types of ***microarray*** slides were fabricated, one contg. 5534 ESTs from 10-14-day-old endosperm, and the other 4844 ESTs from immature ear, estd. to represent about 2800 and 2500 unique genes, resp. Each ***array*** type was hybridized with fluorescent cDNA targets prepd. from endosperm and immature ear ***poly*** (***A***)+ RNA. Although the 10-14-day-old postpollination endosperm TUGs showed only 12% overlap with immature ear TUGs, endosperm target hybridized with 94% of the ear TUGs, and ear target hybridized with 57% of the endosperm TUGs. Incomplete EST sampling of low-abundance transcripts contributes to an underest. of shared gene expression profiles. Reassembly of ESTs at the criterion of 90% identity suggests how cross hybridization among gene family members can overest. the overlap in genes expressed in ***microarray*** hybridization expts. [This abstr. record is one of fifteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 45 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:234554 CAPLUS <<LOGINID::20061115>>
DN 137:165293
TI PABP1 identified as an arginine methyltransferase substrate using high-density protein ***arrays***
AU Lee, Jaeho; Bedford, Mark T.
CS Science Park-Research Division, The University of Texas M.D. Anderson Cancer Center, Smithville, TX, 78957, USA
SO EMBO Reports (2002), 3(3), 268-273 CODEN: ERMEAX; ISSN: 1469-221X
PB Oxford University Press
DT Journal
LA English
AB The arginine methyltransferases CARM1 and PRMT1 assoc. with the p160 family of nuclear hormone receptor coactivators. This assocn. enhances transcriptional activation by nuclear receptors. We describe a method for identifying arginine N-methyltransferase substrates using ***arrayed*** high-d. protein membranes to perform solid-phase supported enzyme reactions in the presence of the Me donor S-adenosyl-L-methionine. Using this screen, we identified distinct substrates for CARM1 and PRMT1. All PRMT1 substrates harbor the expected GGRGG methylation motif, whereas the peptide sequence comparisons of the CARM1 substrates revealed no such motif. The predominant CARM1 substrate identified in this screen was PABP1. We mapped the methylated region of this RNA binding mol. in vitro and demonstrate that PABP1 is indeed methylated in vivo. Prior to these findings, the only known substrate for CARM1 was histone H3. We broaden the no. of

CARM1 targets and suggest a role for CARM1 in regulating transcription/translation.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 46 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:225951 CAPLUS <<LOGINID::20061115>>
DN 136:242716
TI Comparison of RNA expression profiles based on maize expressed sequence tag frequency analysis and micro-***array*** hybridization
AU Fernandes, John; Brendel, Volker; Gai, Xiaowu; Lal, Shailesh; Chandler, Vicki L.; Elumalai, Rangasamy P.; Galbraith, David W.; Pierson, Elizabeth A.; Walbot, Virginia
CS Department of Biological Sciences, Stanford University, Stanford, CA, 94305-5020, USA
SO Plant Physiology (2002), 128(3), 896-910 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Assembly of 73,000 expressed sequence tags (ESTs) representing multiple organs and developmental stages of maize (Zea mays) identified .apprx.22,000 tentative unique genes (TUGs) at the criterion of 95% identity. Based on sequence similarity, overlap between any two of 9 libraries with >3000 ESTs ranged from 4 to 20% of the constituent TUGs. The most abundant ESTs were recovered from only one or a minority of the libraries, and only 26 EST contigs had members from all nine EST sets (presumably representing ubiquitously expressed genes). For several examples, ESTs for different members of gene families were detected in distinct organs. To study this further, 2 types of ***microarray*** slides were fabricated, one contg. 5534 ESTs from 10-14-day-old endosperm, and the other 4844 ESTs from immature ear, estd. to represent about 2800 and 2500 unique genes, resp. Each ***array*** type was hybridized with fluorescent cDNA targets prepd. from endosperm and immature ear ***poly*** (***A***)+ RNA. Although the 10-14-day-old postpollination endosperm TUGs showed only 12% overlap with immature ear TUGs, endosperm target hybridized with 94% of the ear TUGs, and ear target hybridized with 57% of the endosperm TUGs. Incomplete EST sampling of low-abundance transcripts contributes to an underest. of shared gene expression profiles. Reassembly of ESTs at the criterion of 90% identity suggests how cross hybridization among gene family members can overest. the overlap in genes expressed in ***microarray*** hybridization expts. [This abstr. record is one of fifteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 47 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:214668 CAPLUS <<LOGINID::20061115>>
DN 137:150359
TI Identification of genes regulated by dexamethasone in multiple myeloma cells using oligonucleotide ***arrays***
AU Chauhan, Dharminder; Auclair, Daniel; Robinson, Elisabeth K.; Hideshima, Teru; Li, Guilan; Podar, Klaus; Gupta, Deepak; Richardson, Paul; Schlossman, Robert L.; Krett, Nancy; Chen, Lan Bo; Munshi, Nikhil C.; Anderson, Kenneth C.
CS The Jerome Lipper Multiple Myeloma Center, Department of Adult Oncology, Dana Farber Cancer Institute, Harvard Medical School, Boston, MA, 02115, USA
SO Oncogene (2002), 21(9), 1346-1358 CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
AB Our previous studies have characterized Dexamethasone (Dex)-induced apoptotic signaling pathways in multiple myeloma (MM) cells; however, related transcriptional events are not fully defined. In the present study, gene expression profiles of Dex-treated MM cells were detd. using oligonucleotide ***arrays*** . Dex triggers early transient induction of many genes involved in cell defense/repair-machinery. This is followed by induction of genes known to mediate cell death and repression of growth/survival-related genes. The mol. and genetic alterations assocd. with Dex resistance in MM cells are also unknown. We compared the gene expression profiles of Dex-sensitive and Dex-resistant MM cells and identified a no. of genes which may confer Dex-resistance. Finally, gene profiling of freshly isolated MM patient cells validates our in vitro MM cell line data, confirming an in vivo relevance of these studies. Collectively, these findings provide insights into the basic mechanisms of Dex activity against MM, as well as mechanisms of Dex-resistance in MM cells. These studies may therefore allow improved therapeutic uses of Dex, based upon targeting genes that regulate MM cell growth and survival.
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 48 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:204411 CAPLUS <<LOGINID::20061115>>
DN 137:211565
TI Identification of brassinosteroid responsive genes in Arabidopsis by cDNA ***array***
AU Hu, Yuxin; Wang, Zhengke; Wang, Yonghong; Bao, Fang; Li, Ning; Peng, Zhenhua; Li, Jiayang
CS Institute of Genetics, Chinese Academy of Sciences, Beijing, 100101, Peop. Rep. China
SO Science in China, Series C: Life Sciences (2001), 44(6), 637-643 CODEN: SCCLFO; ISSN: 1006-9305
PB Science in China Press
DT Journal
LA English
AB We have systematically monitored brassinosteroid (BR) responsive genes in a BR-deficient mutant det2 suspension culture of Arabidopsis by using a cDNA ***array*** approach. Among 13000 cDNA clones ***arrayed*** on filters, 53 BR responsive clones were identified and designated BRR1-BRR53. Sequence anal. of 43 clones showed that 19 clones are novel genes, 3 clones are genes involved in the control of cell division, 4 clones are genes related to plant stress responses, 4 clones are transcriptional factor or signal transduction component genes, and 3 clones are genes involved in RNA splicing or structure forming. In addn., we also found that BR regulated the transcription of genes related to many physiol. processes, such as photoreaction, ion transportation and some metabolic processes. These findings present mol. evidence that BR plays an essential role in plant growth and development.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 49 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:199899 CAPLUS <<LOGINID::20061115>>
DN 137:227264
TI Assessment of the gene expression profile of differentiated and dedifferentiated human fetal chondrocytes by ***microarray*** analysis
AU Stokes, David G.; Liu, Gang; Coimbra, Ibsen B.; Piera-Velazquez, Sonsoles; Crowl, Robert M.; Jimenez, Sergio A.
CS Jefferson Medical College, Thomas Jefferson University, Philadelphia, PA, USA
SO Arthritis & Rheumatism (2002), 46(2), 404-419 CODEN: ARHEAW; ISSN: 0004-3591
PB Wiley-Liss, Inc.
DT Journal
LA English
AB The purpose of this study was to study the changes in patterns of gene expression exhibited by human chondrocytes as they dedifferentiate into fibroblastic cells in culture to better understand the mechanisms that control this process and its relation to the phenotypic changes that occur in chondrocytes during the development of osteoarthritis (OA). Human fetal epiphyseal chondrocytes (HFCs) were cultured either on poly-(2-hydroxyethyl methacrylate)-coated plates (differentiated HFC cultures) or in plastic tissue culture flasks as monolayers (dedifferentiated HFC cultures). Following 11 days of culture under either condition, ***poly*** (***A*** +) RNA was isolated from the two cell populations and subjected to a gene expression anal. using a ***microarray*** contg. .apprx.5,000 known human genes and .apprx.3,000 expressed sequence tags (ESTs). A .gtoreq.2-fold difference in the expression of 62 known genes and 6 ESTs was obsd. between the two cell types. The differences in expression of several of the genes detected by the ***microarray*** hybridization were confirmed by Northern analyses. Two transcription factor genes, TWIST and HIF-1.alpha., and a cellular adhesion protein gene, cadherin 11, were markedly regulated in response to differentiation and dedifferentiation. Expression of these genes was also detected in adult normal and OA cartilage and chondrocytes. Anal. of the gene expression profile of HFCs revealed a complex pattern of gene expression, including many genes not yet reported to be expressed by chondrocytes. Chondrocytes in monolayer become dedifferentiated, acquiring a fibroblast-like appearance and changing their pattern of gene expression from one of expression of chondrocyte-specific genes to one that resembles a fibroblastic or chondroprogenitor-like pattern. Changes in gene expression assocd. with the process of dedifferentiation of HFCs in vitro were obsd. in a wide variety of genes, including genes encoding extracellular matrix proteins, transcription factors, and growth factors. At least 3 of the genes that were regulated in response to dedifferentiation were also expressed in adult normal and OA articular cartilage and chondrocytes.
RE.CNT 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 50 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:43345 CAPLUS <<LOGINID::20061115>>
DN 136:319709
TI Transcriptional profiling reveals global defects in energy metabolism, lipoprotein, and bile acid synthesis and transport with reversal by leptin treatment in Ob/ob mouse liver
AU Liang, Chien-Ping; Tall, Alan R.
CS Division of Molecular Medicine, Department of Medicine, Columbia University, New York, NY, 10032, USA
SO Journal of Biological Chemistry (2001), 276(52), 49066-49076 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Leptin, a hormone secreted by adipose tissue, has been shown to have a major influence on hepatic lipid and lipoprotein metab. To characterize changes in lipid and lipoprotein gene expression in mouse liver, suppression subtractive hybridization and cDNA ***microarray*** anal. were used to identify mRNAs differentially expressed after leptin treatment of ob/ob mice. Ob/ob mice showed a profound decrease in mRNAs encoding genes controlling bile acid synthesis and transport as well as a variety of apolipoprotein genes and hepatic lipase with reversal upon leptin administration, suggesting that leptin coordinately regulates high d. lipoprotein and bile salt metab. Leptin administration also resulted in decreased expression of genes involved in fatty acid and cholesterol synthesis, glycolysis, gluconeogenesis, and urea synthesis, and increased expression of genes mediating fatty acid oxidn., ATP synthesis, and oxidant defenses. The changes in mRNA expression are consistent with a switch in energy metab. from glucose utilization and fatty acid synthesis to fatty acid oxidn. and increased respiration. The latter changes may produce oxidant stress, explaining the unexpected finding that leptin induces a battery of genes involved in antioxidant defenses. Expression cluster anal. revealed responses of several sets of genes that were kinetically linked. Thus, the mRNA levels of genes involved in fatty acid and cholesterol synthesis are rapidly (<1 h) repressed by leptin administration, in assocn. with an acute decrease in plasma insulin levels and decreased sterol regulator element-binding protein-1 expression. In contrast, genes participating in fatty acid oxidn. and ketogenesis were induced more slowly (24 h), following an increase in expression of their common regulatory factor, peroxisome proliferator-activated receptor .alpha.. However, the regulation of genes involved in high d. lipoprotein and bile salt metab. shows complex kinetics and is likely to be mediated by novel transcription factors.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 51 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:5500 CAPLUS <<LOGINID::20061115>>
DN 136:381200
TI Gene expression analyzed by ***microarrays*** in HSV-1 latent mouse trigeminal ganglion following heat stress
AU Hill, James M.; Lukiw, Walter J.; Gebhardt, Bryan M.; Higaki, Shiro; Loutsch, Jeannette M.; Myles, Marvin E.; Thompson, Hilary W.; Kwon, Byoung S.; Bazan, Nicolas G.; Kaufman, Herbert E.
CS Department of Ophthalmology, Department of Pharmacology, Department of Microbiology, LSU Eye Center, The LSU Neuroscience Center, New Orleans, LA, 70112, USA
SO Virus Genes (2001), 23(3), 273-280 CODEN: VIGEET; ISSN: 0920-8569
PB Kluwer Academic Publishers
DT Journal
LA English
AB An understanding of the cellular genes whose expression is altered during HSV reactivation will enable us to better understand host responses and biochem. pathways involved in the process. Furthermore, this knowledge could allow us to develop gene-targeted inhibitors to prevent viral reactivation.

Mice latent with HSV-1 strain McKrae and uninfected control mice were subjected to hyperthermic stress (43.degree.C for 10 min) and their trigeminal ganglia (TG) collected 1 h later. Two addnl. groups included HSV-1 latently infected and uninfected mice not subjected to hyperthermic stress. ***Poly*** ***A*** + mRNA was enriched from total mouse TG RNA and reverse transcribed using MMLV RT. Radioactively labeled cDNAs were analyzed by ***microarray*** anal. A stress/toxicol. ***array*** of 149 mouse genes on a nylon membrane was used. The labeled cDNAs prepd. from latently infected, stressed mice demonstrated 3-fold or greater increases in certain mRNA-early response genes (ERGs) compared to cDNAs from uninfected, stressed control mice. The ERG mRNAs that showed increases included two heat shock proteins (HSP60 and HSP40), a basic transcription factor (BTF T62), a DNA repair enzyme, two kinases [MAP kinase and a stress-induced protein kinase (SADK)], an oxidative stress-induced protein, a manganese superoxide dismutase precursor-2 (SOD-2), and cyclooxygenase 2 (COX-2). The gene expression in unstressed, infected TGs was similar to the gene expression in unstressed, uninfected controls. These results suggest that there is a significant difference in the ERG expression profile in latently infected TGs undergoing stress-induced reactivation compared to uninfected TGs.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 52 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:2050 CAPLUS <<LOGINID::20061115>>
DN 136:291812
TI Sugarcane ESTs differentially expressed in immature and maturing internodal tissue
AU Carson, Deborah L.; Huckett, Barbara I.; Botha, Frederik C.
CS Biotechnology Department, South African Sugar Association Experiment Station, Mount Edgecombe, 4300, S. Afr.
SO Plant Science (Shannon, Ireland) (2002), 162(2), 289-300 CODEN: PLSCE4; ISSN: 0168-9452
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Two subtracted cDNA libraries were constructed by reciprocal subtractive hybridization between sugarcane immature (low sucrose-accumulating) and maturing (high sucrose-accumulating) internodal tissue. The subtracted libraries contained high, moderate and low abundance transcripts. To isolate cDNAs differentially expressed during culm maturation, 400 random clones (200 from each library) were systematically ***arrayed*** onto nylon filters and screened with total cDNA probes prepd. from immature and maturing culm ***poly*** (***A***)+ RNA. Results indicated that 36 and 30% of the total no. of cDNAs analyzed were preferentially expressed in the immature and maturing culm, resp. Northern anal. of selected clones confirmed culm developmental stage-specific and -preferential expression for most of the clones tested. Expressed Sequence Tags (ESTs) generated by partial sequence anal. for all 132 differentially expressed clones indicated 95 unique transcripts. Partial sequence information could assign putative identities to 66% of the differentially expressed ESTs. The majority of ESTs with a putative identity were homologous to genes assocd. with cell wall metab., carbohydrate metab., stress responses and regulation, where the specific ESTs identified in the immature and maturing culm were distinct from each other. No developmentally regulated ESTs directly assocd. with sucrose metab. were detected. This suggests that growth and maturation of the sugarcane culm is assocd. with the expression of genes for a variety of processes. This study demonstrates that a combination of cDNA subtraction with macroarray screening is an effective strategy to identify and analyze candidate developmentally regulated genes in sugarcane.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 53 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:936053 CAPLUS <<LOGINID::20061115>>
DN 136:49323
TI Substrate on metal film as self-assembled monolayer and method of detecting nucleic acid base sequences
IN Nakamura, Fumio; Hara, Masahiko
PA Riken, Japan
SO U.S. Pat. Appl. Publ., 10 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 2001055768 A1 20011227 US 2001-853948 20010511 US 6495328 B2 20021217 JP 2002051774 A2 20020219 JP 2001-73028 20010314
PRAI JP 2000-161289 A 20000530 JP 2001-73028 A 20010314
OS MARPAT 136:49323
AB A substrate for detecting base sequences that comprises a transparent support, a thin metal film formed on one side of the transparent support, and a self-assembled monolayer with a nonionic arom. compd. being an intercalator of nucleic acid polymers dispersed over the surface formed on the metal film. The substrate is manufd., for example, by immersing a transparent support with a thin gold film formed on one side in a soln. that contains a disulfide (S-S) compd. contg. anthracene for the intercalator of nucleic acid polymers form on the metal film. A nucleic acid polymer (probe or target) is immobilized to the monolayer of the substrate, another nucleic acid polymer (target or probe) is hybridized to the nucleic acid polymer immobilized to the monolayer, and the results of the hybridization can be detected by the Surface Plasmon Resonance method after washing.

L12 ANSWER 54 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:849246 CAPLUS <<LOGINID::20061115>>
DN 136:338052
TI Gene profiling of human fetal and adult adrenals
AU Rainey, W. E.; Carr, B. R.; Wang, Z-N.; Parker, C. R., Jr.
CS Department of Obstetrics and Gynecology, Division of Reproductive Endocrinology, Southwestern Medical Center, University of Texas, Dallas, TX, 75390, USA
SO Journal of Endocrinology (2001), 171(2), 209-215 CODEN: JOENAK; ISSN: 0022-0795
PB Society for Endocrinology
DT Journal
LA English
AB The mechanisms that lead to the steroidogenic differences in the human fetal adrenal (HFA) and adult adrenal gland are not known. However, gene expression clearly plays a crit. role in defining their distinct steroidogenic and structural phenotypes. We used DNA ***microarrays*** to compare expression levels of several thousand transcripts between the HFA and adult adrenal gland. Total RNA was isolated from 18 HFA and 12 adult adrenal glands. Samples of total RNA were used to make five

pools of ***poly*** ***A*** + RNA (mRNA). Gene profiling was done using five independent ***microarrays*** that contained between 7075 and 9182 cDNA elements. Sixty-nine transcripts were found to have a greater than 2.5-fold difference in expression between HFA and adult adrenals. The largest differences were obsd. for transcripts that encode IGF-II (25-fold higher in HFA) and 3.beta.-hydroxysteroid dehydrogenase (24-fold higher in adult). Among the other genes, transcripts related to sterol biosynthesis or to growth and development were higher in the HFA than adult adrenals. Transcripts concerned with cellular immunity and signal transduction were preferentially expressed in the adult adrenal. The vast majority of the 69 transcripts have not been studied with regard to adrenal function. Thus, these gene profiles provide valuable information that could help define the mechanisms that control adrenal function.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 55 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:835144 CAPLUS <<LOGINID::20061115>>
DN 136:353322
TI Frequent up-regulation of WNT2 in primary gastric cancer and colorectal cancer
AU Katoh, Masaru
CS Genetics and Cell Biology Section, Genetics Division, National Cancer Center Research Institute, Tokyo, 104-0045, Japan
SO International Journal of Oncology (2001), 19(5), 1003-1007 CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB WNT2 is one of proto-oncogenes with the potential to activate the WNT - .beta.-catenin - TCF signaling pathway, which is most homologous to WNT2B among members of the human WNT gene family. Here, expression of WNT2 mRNA was comprehensively investigated. WNT2 mRNAs were highly expressed in fetal lung, and weakly expressed in placenta. Among 2.0-, 2.9-, 4.1-, and 6.0-kb WNT2 mRNAs, the 2.0-kb WNT2 mRNA was the major transcript in fetal lung. In 3 cases of prostate cancer and 1 case each of lung cancer and cervical cancer, WNT2 was over-expressed in non-cancerous portion as well as in primary tumor. WNT2 was up-regulated in 14 out of 18 cases of primary colorectal cancer, 4 out of 7 cases of uterus tumor, 2 out of 9 cases of breast cancer, and in 2 out of 14 cases of kidney tumor. Up-regulation of WNT2 was also detected in 4 out of 8 cases of primary gastric cancer by expression ***array*** filter hybridization, and in 10 out of another 10 cases of primary gastric cancer by cDNA-PCR. Frequent up-regulation of WNT2 in primary gastric cancer and colorectal cancer might play a key role in carcinogenesis through activation of the WNT - .beta.-catenin - TCF signaling pathway.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 56 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:791002 CAPLUS <<LOGINID::20061115>>
DN 136:100272
TI cDNA ***array*** analysis of cag pathogenicity island-associated Helicobacter pylori epithelial cell response genes
AU Cox, Joanne M.; Clayton, Christopher L.; Tomita, Toshihiko; Wallace, Don M.; Robinson, Philip A.; Crabtree, Jean E.
CS Molecular Medicine Unit, St. James's University Hospital, Leeds, LS9 7TF, UK
SO Infection and Immunity (2001), 69(11), 6970-6980 CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English
AB Helicobacter pylori strains contg. the cag pathogenicity island (PAI) induce NF-.kappa.B activation and interleukin-8 secretion in gastric epithelial cells. The aim of this study was to investigate changes in epithelial gene expression induced by cag PAI-pos. and -neg. strains of H. pylori using high-d. cDNA ***array*** hybridization technol. Radiolabeled cDNA prepd. from H. pylori-infected Kato 3 gastric epithelial cells was hybridized to high-d. cDNA ***arrays*** to identify changes in epithelial gene expression compared to noninfected controls. In vivo expression of selected, differentially expressed genes was examd. by reverse transcription-PCR anal. of H. pylori-pos. and -neg. gastric mucosa. Screening of .apprx.57,800 cDNAs identified 208 known genes and 48 novel genes and/or expressed sequence tags of unknown function to be differentially expressed in Kato 3 cells following H. pylori infection. Marked differences in gene expression profiles were obsd. following cag PAI-pos. and cag PAI-neg. infection with 15 novel cDNAs and 92 known genes being differentially expressed. H. pylori was found to change the expression of genes encoding growth factors and cytokine/chemokines and their receptors, apoptosis proteins, transcription factors and metalloprotease-disintegrin proteins (ADAMs), and tissue inhibitors of metalloproteinases. Gastric differential expression of selected known genes (amphiregulin and ADAM 10) and a novel gene (HPYR1) was confirmed in vivo in patients with H. pylori infection. Confirmation of the in vivo expression of selected genes demonstrates the usefulness of this approach for investigating pathogen-induced changes in host gene expression.
RE.CNT 81 THERE ARE 81 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 57 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:775265 CAPLUS <<LOGINID::20061115>>
DN 136:132090
TI Investigation of differentially expressed genes during the development of mouse cerebellum
AU Kagami, Yoshihiro; Furuichi, Teiichi
CS Laboratory for Molecular Neurogenesis, Brain Science Institute, RIKEN, Wako, 351-0198, Japan
SO Gene Expression Patterns (2001), 1(1), 39-59 CODEN: GEPEAD; ISSN: 1567-133X
PB Elsevier Science B.V.
DT Journal
LA English
AB Before the discovery of DNA ***microarray*** and DNA chip technol., the expression of only a small no. of genes could be analyzed at a time. Currently, such technol. allows us the simultaneous anal. of a large no. of genes to systematically monitor their expression patterns that may be assocd. with various biol. phenomena. We utilized the Affymetrix GeneChip Mu11K to analyze the gene expression profile in developing mouse cerebellum to assist in the understanding of the genetic basis of cerebellar development in mice. Our anal. showed 81.6% (10.321/12.654) of the genes represented on the GeneChip were expressed in the postnatal cerebellum, and among those, 8.7% (897/10.321) were differentially expressed with more than a two-fold change in their max. and min.

expression levels during the developmental time course. Further anal. of the differentially expressed genes that were clustered in terms of their expression patterns and the function of their encoded products revealed an aspect of the genetic foundation that lies beneath the cellular events and neural network formation that takes place during the development of the mouse cerebellum.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 58 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:760989 CAPLUS <<LOGINID::20061115>>
DN 136:364248
TI Gene expression analysis using the RLCS method
AU Suzuki, Harukazu
CS Genome Science Research Center, Institute of Physical and Chemical Research, Japan
SO Daikibo Genomu Kaiseki Gijutsu to Posuto Shikensu Jidai no Idenshi Kino Kaiseki (2001), 168-173. Editor(s): Shinagawa, Akira; Suzuki, Harukazu. Publisher: Nakayama Shoten, Tokyo, Japan. CODEN: 69BXSR
DT Conference; General Review
LA Japanese
AB A review described a cDNA display method based on the application of the restriction landmark scanning technol. Exptl. protocols of the restriction landmark cDNA scanning (RLCS) method were presented by covering the procedures for selection of restriction endonucleases, ***poly*** ***A*** RNA prepn., cDNA synthesis, designing biotinylated oligo (dT) primers contg. specific restriction endonuclease cleaving sites, recovering fragments by streptavidin-immobilized magnetic beads, electrophoresis and in-gel restriction endonuclease digestion. Protocols of cloning procedures for spots of interest (spot cloning) were also presented. Advantage and disadvantage of the application of the RLCS method to gene expression profiling expts. were also discussed by comparing with other methods such as the differential display method and DNA ***microarray*** methods.

L12 ANSWER 59 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:750592 CAPLUS <<LOGINID::20061115>>
DN 136:277222
TI Identification of candidate genes in ulcerative colitis and Crohn's disease using cDNA ***array*** technology
AU Uthoff, Sonja M. S.; Eichenberger, M. Robert; Lewis, Robert K.; Fox, Matthew P.; Hamilton, Crystal J.; Mcauliffe, Tracy L.; Grimes, H. Leighton; Galandiuk, Susan
CS Digestive Surgery Research Laboratory, Department of Surgery, University of Louisville School of Medicine, Louisville, KY, USA
SO International Journal of Oncology (2001), 19(4), 803-810 CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB Inflammatory bowel disease (IBD) follows a multigenic mode of inheritance, encompassing the clin. discrete phenotypes of ulcerative colitis (UC) and Crohn's disease (CD). The risk of malignant transformation of the colon increases with the duration and extent of IBD and is particularly high for patients with a longstanding history of UC. We wished to identify candidate genes that might be involved in disease pathogenesis based on functional plausibility and their putative role in IBD carcinogenesis. ***PolyA*** + mRNA prepn. from inflamed intestinal mucosa of patients with a longstanding history of UC and CD was performed with subsequent hybridization of a phosphorus [.alpha.-32P]-dATP-labeled cDNA populations to nucleic acid ***arrays*** . Of 588 different human gene transcripts ***arrayed*** , secreted apoptosis-related protein 1 (Sarp1), frizzled (fz) homologs, and disheveled (dvl) were differentially expressed, being elevated in UC as compared to CD. These genes encode proteins involved in the Wingless-type (Wnt)/ss-catenin signaling pathway. The autonomous expression of Sarp1 and Sarp1-compatible fz receptor genes suggests that the Wnt pathway may be involved in UC carcinogenesis.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 60 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685155 CAPLUS <<LOGINID::20061115>>
DN 136:306157
TI Multichannel expression analysis of submicrogram total RNA samples without enzymatic amplification using a one-day protocol
AU Getts, Robert C.
CS Genisphere Inc., Montvale, NY, 07645, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 103-111 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB Typical gene expression ***array*** anal. requires relatively large quantities of total or ***poly*** ***A*** +RNA. Samples prepd. by techniques such as laser capture microdissection (LCM) and single cell expression anal. yield relatively little RNA and traditionally require the purifn. of ***poly*** ***A*** + message and subsequent enzymic amplification before anal. on an ***array*** . This type of anal. may be biased to the detection of certain messages, is labor intensive, time consuming and requires considerable expertise for reproducible success. The 3DNA Submicro expression detection kit has been developed to detect low level expression from a microgram or less of total RNA in one day. The method does not require enzymic amplification or the direct incorporation of a modified nucleotide during probe synthesis and is simple and easy to use. The 3DNA detection system is based on patented DNA dendrimers that contain hundreds of fluorescent labels. Signal is generated by the dendrimer after it binds to the cDNA probe (sample) via hybridization of the dendrimer to a capture sequence that is part of the original reverse transcription primer. Fifty-200 fold improvement of specific signal over noise compared to direct incorporation methods has been demonstrated. The theory and use of the 3DNA Submicro technol. will be discussed for 2, 3 and 4 channel anal.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 61 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685153 CAPLUS <<LOGINID::20061115>>
DN 136:350869
TI Designing oligo libraries taking alternative splicing into account
AU Shoshan, Avi; Grebinskiy, Vladimir; Magen, Avner; Scolnicov, Ariel; Fink, Eyal; Lehavi, David; Wasserman, Alon
CS Compugen Inc., Jamesburg, NJ, 08831, USA

SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 86-95 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB We have designed sequences for DNA ***microarrays*** and oligo libraries, taking alternative splicing into account. Alternative splicing is a common phenomenon, occurring in more than 25% of the human genes. In many cases, different splice variants have different functions, are expressed in different tissues or may indicate different stages of disease. When designing sequences for DNA ***microarrays*** or oligo libraries, it is very important to take into account the sequence information of all the mRNA transcripts. Therefore, when a gene has more than one transcript (as a result of alternative splicing, alternative promoter sites or alternative ***poly*** - ***adenylation*** sites), it is very important to take all of them into account in the design. We have used the LEADS transcriptome prediction system to cluster and assemble the human sequences in GenBank and design optimal oligonucleotides for all the human genes with a known mRNA sequence based on the LEADS predictions.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 62 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:613076 CAPLUS <<LOGINID::20061115>>
DN 136:213260
TI RNAs extracted from herpes simplex virus 1 virions: apparent selectivity of viral but not cellular RNAs packaged in virions
AU Sciortino, Maria-Teresa; Suzuki, Mikiko; Taddeo, Brunella; Roizman, Bernard
CS The Marjorie B. Kovler Viral Oncology Laboratories, The University of Chicago, Chicago, IL, 60637, USA
SO Journal of Virology (2001), 75(17), 8105-8116 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB Following the lead of recent studies on the presence of RNA in virions of human cytomegalovirus, we investigated the presence and identity of RNAs from purified virions of herpes simple virus 1. To facilitate these studies, we designed primers for all known open reading frames (ORFs) and also constructed cDNA ***arrays*** contg. probes designed to detect all known transcripts. In the first series of expts., labeled DNA made by reverse transcription of ***poly*** (***A***)+ RNA extd. from infected HEp-2 or rabbit skin cells hybridized to all but two of the probes in the cDNA ***array*** . A similar anal. of the RNA extd. from purified extracellular virions derived from infected HEp-2 cells hybridized to probes representing 24 of the ORFs. In the second series of analyses, we reverse transcribed and amplified by PCR RNAs from purified intracellular or extracellular virions derived from infected HEp-2 or Vero cell lines. The pos. RNAs were retested by PCR with and without prior reverse transcription to ensure that the samples tested were free of contaminating DNA. The results were as follows. (i) Only a fraction of viral ORF transcripts were represented in virion RNA, and only nine RNAs (UL10, UL34/UL35, UL36, UL42, UL48, UL51, US1/US1.5, US8.5, and US10/US11) were pos. in all RT PCR assays. Of these, seven were pos. by hybridization to cDNA ***arrays*** . (ii) RNA extd. from cells infected with a mutant virus lacking the US8 to US12 genes yielded results similar to those described above, indicating that US11, a known RNA binding protein, does not play a role in packaging RNA in virions. (iii) Cellular RNAs detected in virions were representative of the abundant cellular RNAs. Last, RNA extd. from virions was translated in vitro and the translation products were reacted with antibody to .alpha.TIF (VIP16). The immune ppt. contained a labeled protein with the apparent mol. wt. of .alpha.TIF, indicating that at least one mRNA packaged in virions was intact and capable of being translated. The basis for the apparent selectivity in the packaging of the viral RNAs packaged in virions is unknown.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 63 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:590631 CAPLUS <<LOGINID::20061115>>
DN 136:211383
TI Application of fluorescently labeled poly(dU) for gene expression profiling on cDNA microarays
AU Meiyanto, Edy; Mineno, Jun-Ichi; Ishida, Norihiro; Takeya, Tatsuo
CS Nara Institute of Science and Technology, Nara, 630-0101, Japan
SO BioTechniques (2001), 31(2), 406-408, 410, 412-413 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB The membrane filter hybridization technique has been widely used for gene expression profiling. The prepn. of sensitive and reliable probes is crit. for quant. anal. in this technique. We report a method in which fluorescently labeled poly(dU) is used to detect ***poly*** (***A***)-contg. mRNA that hybridizes to specific gene targets. The probe can be used commonly for every sample, alleviating problems encountered in prepg. cDNA probes by reverse transcription, particularly when many samples are to be analyzed. Moreover, the sensitivity is at least comparable to cDNA probes prepd. by conventional protocols, and intensities of signals after hybridization are independent of mRNA sizes and solely dependent on copy nos. This method was also shown to be applicable to DNA chip technol.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 64 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:582090 CAPLUS <<LOGINID::20061115>>
DN 135:163339
TI Method for isolating, identifying and cataloging polynucleotides encoding proteins assocd. with endoplasmic reticulum
IN Landes, Gregory M.
PA Genzyme Corporation, USA
SO PCT Int. Appl., 51 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2001057257 A2 20010809 WO 2001-US3464 20010201 WO 2001057257 A3 20020418 W: AU, CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU,

MC, NL, PT, SE, TR AU 2001034769 A5 20010814 AU 2001-34769 20010201 US 2002146693 A1 20021010 US 2001-773861 20010201
PRAI US 2000-180582P P 20000204 WO 2001-US3464 W 20010201
AB The present invention provides a method for isolating, identifying and cataloging polynucleotides (mRNA, cDNA or gene) encoding secreted proteins assocd. with endoplasmic reticulum. The method requires obtaining a polynucleotide from a cellular homogenate, wherein the polynucleotide encodes said polypeptide, and detg. the sequence of the polynucleotide and its expression level. In essence, the method consists of two phases: (1) enrichment/purifn. of membrane-bound ***poly*** (***A***)-contg. mRNA, and (2) sequence anal. The invention also provides computer-related systems and methods. More specifically, the invention provides a system and method for automatically generating a database of polynucleotides encoding endoplasmic reticulum-assocd. proteins. The invention further provides a gene delivery vehicle comprising said polynucleotide, and a host cell comprising said polynucleotide. Finally, the invention provides antibodies that specifically recognize and bind to said endoplasmic reticulum-assocd. proteins. The invention also related that after enrichment/purifn. of membrane-bound ***poly*** (***A***)-contg. mRNA, a library can be constructed using the purified ***poly*** (***A***)-contg. mRNA to analyze said polynucleotides. The invention further related that a ***poly*** (***A***)-contg. mRNA, that contains a sequence of particular interest, can be identifying by nucleic acid hybridization. The invention further related that differential display, expressed sequence tag, and Serial Anal. of Gene Expression (SAGE) methods can be used to analyze said polynucleotides.

L12 ANSWER 65 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:575720 CAPLUS <<LOGINID::20061115>>
DN 136:277296
TI Transcription of intermediate filament genes is enhanced in focal cortical dysplasia
AU Taylor, J. Paul; Sater, Richard; French, Jacqueline; Baltuch, Gordon; Crino, Peter B.
CS Department of Neurology, University of Pennsylvania Medical Center, Philadelphia, PA, 19104, USA
SO Acta Neuropathologica (2001), 102(2), 141-148 CODEN: ANPTAL; ISSN: 0001-6322
PB Springer-Verlag
DT Journal
LA English
AB Focal cortical dysplasia (FCD) is characterized by disorganized cerebral cortical cytoarchitecture. Increased expression of several intermediate filament (IF) proteins such as neurofilament, vimentin, .alpha.-internexin, and nestin obsd. in dysplastic "balloon" neurons (DN) may contribute to disrupted cortical lamination. We hypothesized that increased IF protein expression results from enhanced IF gene transcription within dysplastic neurons. We used a novel strategy to evaluate IF mRNA expression in three FCD specimens from medically intractable epilepsy patients. ***Poly*** (***A***) mRNA was amplified (aRNA) from single microdissected DN, morphol. normal neurons at the margin of the FCD resection, morphol. normal neurons in non-FCD cortex from epilepsy patients, and normal control neurons. Radiolabeled aRNA from single neurons was used to probe cDNA ***arrays*** contg. the low (NFL), medium (NFM) and high (NFH) mol. wt. neurofilament isoform, .alpha.-internexin, desmin, vimentin, peripherin (PRPH), nestin, and glial fibrillary acidic protein (GFAP) cDNAs. Hybridization intensity of aRNA-cDNA hybrids was used to quantify relative IF abundance. Increased expression of nestin, .alpha.-internexin, PRPH, vimentin, NFL, NFM, and NFH mRNAs was found in DN when compared with the three control neuronal subtypes. Desmin and GFAP mRNAs were not detected in any cell types. Expression of PRPH mRNA and protein in select DN was confirmed by reverse transcription-polymerase chain reaction and immunohistochem. We conclude that aberrant expression of IF proteins in FCD likely results from enhanced transcription of IF genes in dysplastic neurons and propose that future anal. of transcriptional elements that regulate IF expression be evaluated in FCD.
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 66 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:544244 CAPLUS <<LOGINID::20061115>>
DN 135:255313
TI Overexpression of .alpha.4 chain-containing laminins in human glial tumors identified by gene ***microarray*** analysis
AU Ljubimova, Julia Y.; Lakhter, Alexander J.; Loksh, Anna; Yong, William H.; Riedinger, Mary S.; Miner, Jeffrey H.; Sorokin, Lydia M.; Ljubimov, Alexander V.; Black, Keith L.
CS Cedars-Sinai Medical Center, Maxine Dunitz Neurosurgical Institute, Los Angeles, CA, 90048, USA
SO Cancer Research (2001), 61(14), 5601-5610 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Differential gene expression in tumors often involves growth factors and extracellular matrix/basement membrane components. Here, 11,000-gene ***microarray*** was used to identify gene expression profiles in brain tumors including high-grade gliomas [glioblastoma multiforme (GBM) and anaplastic astrocytoma], low-grade astrocytomas, or benign extra-axial brain tumors (meningioma) in comparison with normal brain tissue. Histol. normal tissues adjacent to GBMs were also studied. All GBMs studied overexpressed 14 known genes compared with normal human brain tissue. Overexpressed genes belonged to two broad groups: (a) growth factor-related genes; and (b) structural/extracellular matrix-related genes. For most of these 14 genes, expression levels were lower in low-grade astrocytoma than in GBM and were barely detectable in normal brain. Despite normal-appearing histol., gene expression patterns of tissues immediately adjacent to GBM were similar to those of their resp. primary GBMs. Two genes were consistently up-regulated in both high-grade and low-grade gliomas, as well as in histol. normal tissues adjacent to GBMs. These genes coded for the epidermal growth factor receptor (previously reported to be overexpressed in gliomas) and for the .alpha.4 chain of laminin, a major blood vessel basement membrane component. Changes in expression of this laminin chain have not been previously assocd. with malignant tumors. Overexpression of laminin .alpha.4 chain in GBM and astrocytoma grade II by gene ***microarray*** anal. was confirmed by semiquantitative reverse transcription-PCR and immunohistochem. Importantly, an .alpha.4 chain-contg. laminin isoform, laminin-8 (.alpha.4.beta.1.gamma.1), was expressed mainly in blood vessel walls of GBMs and histol. normal tissues adjacent to GBMs, whereas another .alpha.4 chain-contg. laminin isoform, laminin-9 (.alpha.4.beta.2.gamma.1), was expressed mainly in blood vessel walls of low-grade tumors and normal

brain. GBMs that overexpressed laminin-8 had a shorter mean time to tumor recurrence (4.3 mo) than GBMs with overexpression of laminin-9 (9.7 mo, P = 0.0007). Up-regulation of .alpha.4 chain-contg. laminins could be important for the development of glioma-induced neovascularization and glial tumor progression. Overexpression of laminin-8 may be predictive of glioma recurrence.
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 67 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:508045 CAPLUS <<LOGINID::20061115>>
DN 135:89547
TI Methods of labeling nucleic acids for use in ***array*** based hybridization assays
IN Bochkariov, Dmitry E.; Chenchik, Alex
PA USA
SO U.S. Pat. Appl. Publ., 10 pp., Cont.-in-part of U. S. Ser. No. 424,175. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 4 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 2001007747 A1 20010712 US 1999-454183 19991202 US 6383749 B2 20020507 WO 9853103 A1 19981126 WO 1998-US10561 19980521 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
PRAI WO 1998-US10561 W 19980521 US 2000-424175 A2 20000217 US 1997-859998 A 19970521 US 1998-53375 A 19980331
AB Methods and kits are provided for labeling nucleic acids, e.g. for use in ***array*** based hybridization assays. In the subject methods, target nucleic acid is generated from an initial nucleic acid source, e.g. mRNA, where the target nucleic acid is characterized by having at least one reactive functionality that is not a moiety found on naturally occurring nucleic acids. Functionalized label is then conjugated to the target nucleic acid, either before or after it has been hybridized to ***array*** of nucleic acids stably assocd. with the surface of a solid support. The subject methods find use in a variety of ***array*** based hybridization assays, including differential expression assays. The functionalized label is contacted with the functionalized target under conditions sufficient for conjugation of the label to the target to occur, i.e. for the target and reactive functionalities to react with each other to produce a covalent bond or linkage between the label and the nucleic acid. For example, where the first functionality present on the target is an amino group and the second functionality present on the label is an N-hydroxysuccinimide ester group, the contact conditions are chosen such that a reaction occurs between the amino and N-hydroxysuccinimide ester groups to form a covalent bond between the label and the nucleic acid. Prepn. of Cy3 (Cy3 N-hydroxysuccinimide ester) labeled target nucleic acid (***polyA*** + placental RNA) is described.

L12 ANSWER 68 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:508044 CAPLUS <<LOGINID::20061115>>
DN 135:103341
TI Methods (RT-PCR followed by hybridization) and materials (pool of gene-specific primers) for analyzing differences in mRNA expression profiles
IN Chenchik, Alex; Jokhadze, George; Bibilashvilli, Robert
PA Clontech Laboratories, Inc., USA
SO U.S. Pat. Appl. Publ., 12 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 2001007744 A1 20010712 US 1999-225201 19990105 US 6489455 B2 20021203
PRAI US 1999-225201 19990105
AB The invention provides methods (reverse transcription-polymerase chain reaction (RT-PCR) followed by nucleic acid hybridization) and materials for analyzing differences in the mRNA expression profiles between a plurality of different physiol. samples. The invention specifically discloses a pool of gene-specific primers employed in said PCR, as well as a test kit comprising said primers, along with other materials needed, including probe ***array*** , DNA polymerase, reverse transcriptase and dTNPs. In the example section, the invention outlined the steps involved in the method which included: (1) prodn. of cDNAs from ***polyA*** mRNA using reverse transcriptase; (2) amplification of labeled cDNAs from physiol. sources using gene-specific primers, and (3) detection of labeled target cDNAs generated by PCR using cDNA ***array*** hybridization.

L12 ANSWER 69 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:465883 CAPLUS <<LOGINID::20061115>>
DN 135:208996
TI Molecular profiling of transformed and metastatic murine squamous carcinoma cells by differential display and cDNA ***microarray*** reveals altered expression of multiple genes related to growth, apoptosis, angiogenesis, and the NF-.kappa.B signal pathway
AU Dong, Gang; Loukinova, Elena; Chen, Zhong; Gangi, Lisa; Chanturita, Tatyana I.; Liu, Edison T.; Van Waes, Carter
CS Head and Neck Surgery Branch, National Institute on Deafness and Other Communication Disorders/NIH, Bethesda, MD, 20892, USA
SO Cancer Research (2001), 61(12), 4797-4808 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB To identify changes in gene expression with transformation and metastasis, we investigated differential gene expression in a squamous carcinoma model established in syngeneic mice. We used mRNA differential display (DD) to detect global differences and cDNA ***arrays*** enriched for cancer-assocd. genes using mRNA from primary keratinocytes, transformed Pam 212 squamous carcinoma cells, and metastases of Pam 212. After DD, 72 candidate cDNAs expressed primarily in transformed and metastatic cells were selected and cloned. Fifty-seven were detected, and 32 were confirmed to be differentially expressed by Northern blot anal. MRNA expression profiles were also generated using a mouse cDNA ***array*** composed of 4000 elements representing known genes and expressed

sequence tags plus the 57 DD candidate cDNAs detected by Northern anal. to facilitate data validation. CDNA ***array*** detected 76.9% of the differentially expressed mRNAs selected from DD and confirmed by Northern blot, whereas low-abundance mRNAs did not reach the threshold for detection by the lower-sensitivity ***array*** method. Clustering anal. of DD and ***array*** results from transformed and metastatic cells identified genes that exhibited decreased or increased expression with transformation and metastasis. Alterations in the expression of several genes detected during tumor progression were consistent with their functional activities involving growth (p21, p27, and cyclin D1), resistance and apoptosis (glutathione-S-transferase, cIAP-1, PEA-15, and Fas ligand), inflammation and angiogenesis [chemokine growth-regulated oncogene 1 (also called KC)], and signal transduction (c-Met, yes-assocd. protein, and syk). Strikingly, 10 of 22 genes in the cluster expressed in metastases have been assocd. with activation of the nuclear factor (NF)-.kappa.B signal pathway. The NF-.kappa.B-inducible cytokine Gro-1 was recently shown to promote tumor growth, metastasis, and angiogenesis of squamous cell carcinomas in vivo. The results demonstrate that early response genes related to NF-.kappa.B contribute to metastatic tumor progression. Comparison of cell lines and tumor tissue revealed a concordance of .apprx.50% by ***array*** , and 70% for Northern-confirmed, metastasis-related genes. Functional genomic approaches comparing expression among cell lines and tumor tissue may promote a better understanding of the genes expressed by malignant and host cells during tumor progression and metastasis.
RE.CNT 87 THERE ARE 87 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 70 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:464576 CAPLUS <<LOGINID::20061115>>
DN 135:90355
TI Senescence-related changes in gene expression in muscle: similarities and differences between mice and men
AU Welle, Stephen; Brooks, Andrew; Thornton, Charles A.
CS Departments of Medicine, Pharmacology and Physiology, University of Rochester, Rochester, NY, 14642, USA
SO Physiological Genomics [online computer file] (2001), 5(2), 67-73 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/5/2/67
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB A ***microarray*** study of the effect of senescence in mice on gene expression in muscle has been published recently. The present anal. was done to evaluate the extent to which the age-related differences in gene expression in murine muscle are also evident in human muscle. RNA extd. from muscle of young (21-24 yr) and old men (66-77 yr) was studied both by serial anal. of gene expression (SAGE) and by oligonucleotide ***microarrays*** . SAGE tags were detected for 61 genes homologous to genes reported to be differentially expressed in young and old murine muscle. The ***microarray*** had probe sets for 70 homologous genes. For 17 genes, there was evidence for a similar age-related change in expression in muscles of mice and men. For 32 other genes, there was evidence that the effect of age on the level of expression is not the same in mice and men. There was no evidence that older human muscle has increased expression of the stress response genes that are increased in old murine muscle.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 71 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:354388 CAPLUS <<LOGINID::20061115>>
DN 135:105661
TI Growth and gene expression profile analyses of endometrial cancer cells expressing exogenous PTEN
AU Matsushima-Nishiu, Mieko; Unoki, Motoko; Ono, Kenji; Tsunoda, Tatsuhiko; Minaguchi, Takeo; Kuramoto, Hiroyuki; Nishida, Masato; Satoh, Toyomi; Tanaka, Toshihiro; Nakamura, Yusuke
CS Laboratories of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, 108-8639, Japan
SO Cancer Research (2001), 61(9), 3741-3749 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB The PTEN tumor suppressor gene encodes a multifunctional phosphatase that plays an important role in inhibiting the phosphatidylinositol-3-kinase pathway and downstream functions that include activation of Akt/protein kinase B, cell survival, and cell proliferation. Enforced expression of PTEN in various cancer cell lines decreases cell proliferation through arrest of the cell cycle, accompanied in some cases by induction of apoptosis. We used cDNA ***microarrays*** contg. 4009 cDNAs to examine changes in gene-expression profiles when exogenous PTEN was induced in PTEN-defective cells. The ***microarrays*** and subsequent semiquant. reverse transcription-PCR anal. revealed transcriptional stimulation of 99 genes and repression of 72 genes. Some of the differentially expressed genes already had been implicated in cell proliferation, differentiation, apoptosis, or cell cycle control, e.g., overexpression of PTEN-induced transactivation of cyclin-dependent inhibitor 1B (p27Kip1) and 2B (p15INK4B), members of the TNF receptor family, tumor necrosis factor-assocd. genes, and members of the Notch-signaling and Mad families. To our knowledge this is the first report of transactivation of those genes by PTEN. The genes differentially expressed in our expts. also included many whose correlation with cancer development had not been recognized before. Our data should contribute to a greater understanding of the broad spectrum of ways in which PTEN affects intracellular signaling pathways. Anal. of expression profiles with ***microarrays*** appears to be a powerful approach for identifying anticancer genes and/or disease-specific targets for cancer therapy.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 72 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:352230 CAPLUS <<LOGINID::20061115>>
DN 134:348941
TI Monitoring of gene expression by detecting hybridization to nucleic acid ***arrays*** using anti-heteronucleic acid (anti-HNA) antibodies
IN Linsley, Peter S.; Baeuerle, Patrick
PA Rosetta Inpharmatics, Inc., USA; Tularik Inc.
SO U.S., 18 pp. CODEN: USXXAM
DT Patent
LA English

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------

PI US 6232068 B1 20010515 US 1999-236139 19990122
PRAI US 1999-236139 19990122
AB The present invention relates to compns. and methods for detecting, measuring or monitoring gene expression by detecting hybridization of RNA or RNA mimics to DNA ***arrays*** . The invention provides a sensitive, specific method for detecting hybridization on nucleic acid ***arrays*** using anti-heteronucleic acid (anti-HNA) antibodies to detect of RNA-DNA duplexes on ***arrays*** , preferably DNA ***microarrays*** using RNA probes derived directly from the cell, thus obviating the need for isolation of the ***poly*** (***A***)+fraction. The invention provides methods for simultaneously monitoring the expression of a multiplicity of genes.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 73 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:350418 CAPLUS <<LOGINID::20061115>>
DN 135:342584
TI Differential expression of glutamate and GABA-A receptor subunit mRNA in cortical dysplasia
AU Crino, Peter B.; Duhaime, Anne-Christine; Baltuch, Gordon; White, Ricarda
CS Departments of Neurology, University of Pennsylvania School of Medicine, Philadelphia, PA, 19104, USA
SO Neurology (2001), 56(7), 906-913 CODEN: NEURAI; ISSN: 0028-3878
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB The contribution that dysplastic and heterotopic neurons make to epileptogenesis in focal cortical dysplasia is unknown and the phenotype of these cells may be distinct. The authors hypothesized that the expression of genes encoding glutamatergic (glutamate [GluR] and N-methyl-D-aspartate NMDA receptors [NR]) and .gamma.-aminobutyric acid A receptor (GABAAR) subunits is distinct in dysplastic and heterotopic neurons and that changes in receptor gene expression could be defined in a cell-specific pattern. Single immunohisto-chem. labeled dysplastic and heterotopic neurons were microdissected from human focal cortical dysplasia specimens obtained during epilepsy surgery. Pyramidal neurons were microdissected from postmortem control cortex and from temporal cortex without dysplasia resected during temporal lobectomy. ***Poly*** (***A***) mRNA from single neurons was amplified, radiolabeled, and used to probe cDNA ***arrays*** contg. GluR1-6, NR1A,1B, NR2A-D, and GABAAR.alpha.1-6, and -R.beta.1-3 subunit cDNAs. The relative hybridization intensities of each mRNA-cDNA hybrid were quantified by phosphorimaging. GluR, NR, and GABAAR subunit mRNA expression did not differ between control neurons and nondysplastic epilepsy specimens. Expression of GluR4, NR2B, and NR2C subunit mRNA was increased, and NR2A and GABAAR.beta.1 subunit mRNA was decreased in dysplastic compared with pyramidal and heterotopic neurons. In contrast, GABAAR.alpha.1, -R.alpha.2, and -R.beta.2 as well as GluR1 mRNA levels were reduced in both dysplastic and heterotopic neurons. Thus, differential expression of GluR, NR, and GABAAR mRNA in dysplastic and heterotopic neurons demonstrates cell specific gene transcription changes in focal cortical dysplasia. These results suggest that dysplastic and heterotopic neurons may be pharmacol. distinct and make differential contributions epileptogenesis in focal cortical dysplasia.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 74 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:338762 CAPLUS <<LOGINID::20061115>>
DN 134:362292
TI Methods of determining individual hypersensitivity to a pharmaceutical agent from gene expression profile
IN Farr, Spencer
PA Phase-1 Molecular Toxicology, USA
SO PCT Int. Appl., 222 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------

PI WO 2001032928 A2 20010510 WO 2000-US30474 20001103 WO 2001032928 A3 20020725 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 1999-165398P P 19991105 US 2000-196571P P 20000411
AB The invention discloses methods, gene databases, gene ***arrays*** , protein ***arrays*** , and devices that may be used to det. the hypersensitivity of individuals to a given agent, such as drug or other chem., in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes assocd. with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes assocd. with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an ***array*** of nucleic acid probes for the plurality of genes assocd. with hypersensitivity. The expression of the genes predetd. to be assocd. with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases ***arrays*** and app. useful for identifying hypersensitivity in a subject are also disclosed.

L12 ANSWER 75 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:315063 CAPLUS <<LOGINID::20061115>>
DN 136:64791
TI Profiling of gene expression in individual hematopoietic cells by global mRNA amplification and slot blot analysis
AU Theilgaard-Monch, K.; Cowland, J.; Borregaard, N.

CS Department of Hematology-9322, Granulocyte Research Laboratory, The Finsen Center, Rigshospitalet, University of Copenhagen, Copenhagen, 2100, Den.
SO Journal of Immunological Methods (2001), 252(1-2), 175-189 CODEN: JIMMBG; ISSN: 0022-1759
PB Elsevier Science B.V.
DT Journal
LA English
AB The pattern of expressed genes defines the structure and functional status of cells. Currently, most methods used in gene expression studies depend on large nos. of cells. Thus, their application may be hampered by the heterogeneity of cell populations, and by the low nos. of cells obtainable from in vivo sources. Such drawbacks may be overcome by methods suitable for the profiling of gene expression at the single cell level. We studied whether polymerase chain reaction (PCR) products synthesized from individual cells by global amplification of mRNA were suitable as probes for gene expression anal. For this purpose, cells were subjected to reverse transcription and PCR using sequence independent primers (SIP RT-PCR). The resultant cDNA products were radiolabeled and hybridized to cDNA clones ***arrayed*** on a nylon membrane by vacuum slot blotting (a method referred to as slot blot anal.). The SIP RT-PCR procedure was reproducible and allowed the detection of twofold changes in input RNA copies per cell (range: 80-10.000 copies of an in vitro transcribed ***poly*** (***A***)-tailed RNA/cell). Anal. of total RNA and amplified cDNA, obtained from neutrophil granulocytes and the promyelocytic HL-60 cell line, demonstrated comparable gene expression profiles as measured by Northern blot and slot blot anal. Slot blot anal. of HL-60 cells indicated that individual cells from an apparently homogeneous population have varying expression of specific transcripts, which all contribute to the mRNA phenotype of their population. Interestingly, the genes that were detected in some but not all individual HL-60 cells were those found to peak within 2 days of retinoic acid-induced granulocytic differentiation. This study demonstrates the potential of cDNA, synthesized from individual cells by global amplification of mRNA, as probes for cDNA ***arrays*** .
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 76 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:311270 CAPLUS <<LOGINID::20061115>>
DN 136:64699
TI Subtractive hybridization - genetic takeaways and the search for meaning
AU Byers, Richard J.; Hoyland, Judith A.; Dixon, Janet; Freemont, Anthony J.
CS Laboratory Medicine Academic Group, University of Manchester, Manchester, M13 9PT, UK
SO International Journal of Experimental Pathology (2000), 81(6), 391-404 CODEN: IJEPEI; ISSN: 0959-9673
PB Blackwell Science Ltd.
DT Journal; General Review
LA English
AB A review. Gene expression profiling relies on mRNA extn. from defined cell systems, which in the case of pathol. processes necessarily results in the use of small quantities of tissues, sometimes as little as a few cells. This obviates the use of many systems of gene expression profiling and is best carried out using cDNA amplified by ***poly*** (***A***) reverse transcription polymerase chain reaction, which is capable of generating material representative of all the expressed genes in samples as small as one cell. Anal. of this material using subtractive hybridization compares the genes expressed at different stages of a biol./pathol. process allowing identification of the all the genes upregulated during the process. The identification of the genes present is not dependent on their prior description or on the choice of genes used in a screen and as such the method is ideal for identifying novel genes or unsuspected genes. We have used the method to identify genes involved in normal osteoblastic differentiation and in Paget's disease of bone and it has been widely used to study normal differentiation and pathol. processes in a no. of systems. The method, its applications and its relationship with the other methods of gene expression profiling are reviewed.
RE.CNT 113 THERE ARE 113 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 77 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:283999 CAPLUS <<LOGINID::20061115>>
DN 134:306183
TI Human olfactory receptor and encoding polynucleotide sequences and their use for odorant fingerprinting
IN Bellenson, Joel; Smith, Dexster; Lancet, Doron; Glusman, Gustavo; Fuchs, Tania; Yanai, Itai
PA Digiscents, USA; Yeda Research and Development Co., Ltd.
SO PCT Int. Appl., 1857 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2001027158 A2 20010419 WO 2000-US27582 20001006 WO 2001027158 A3 20020926 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 1999-158615P P 19991008 US 2000-184809P P 20000224
AB The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation and their use in screening for olfactory agonists and antagonists. The polynucleotide sequences were identified using oligonucleotide primers complementary to olfactory receptor membrane-spanning regions to amplify cDNA prepd. from ***poly*** (***A***)+ RNA isolated from human olfactory epithelial tissue. A datamining pipeline was also built to detect all available olfactory receptor-like sequences in the public databases and to update the results as new database versions are released. In addn. to 115 cDNA sequences isolated from human olfactory epithelia, datamining provides 932 olfactory receptor-encoding polynucleotides which are deposited and described in the Human Olfactory Receptor Data Exploratorium (http://www.bioinfo.weizman.ac.il/HORDE). The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences, and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologs of these

polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant mols. to det. the correspondence (scent representation, scent fingerprint, or scent profile) between individual odorant receptors (the polypeptides) and particular odorant mols. Also encompassed by the present invention is the use of the scent representation, scent fingerprint, or scent profile to re-create and edit scents.

L12 ANSWER 78 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:197593 CAPLUS <<LOGINID::20061115>>
TI Genome-wide monitoring of transcriptional response of the yeast, S. cerevisiae, to a bioactive contaminant
AU Xu, Deming; Brooker, Deborah; McNeil, Bryan; McCarry, Brian; Friesen, James D.; Yager, Thomas
CS C.H. Best Microarray Center, BBDMR, University of Toronto, Toronto, ON, M5G 1L6, Can.
SO Abstracts of Papers, 221st ACS National Meeting, San Diego, CA, United States, April 1-5, 2001 (2001) BTEC-018 CODEN: 69FZD4
PB American Chemical Society
DT Journal; Meeting Abstract
LA English
AB Coal tar is a complex mixt. of PAH compds. produced from industrial processes. To assess its bioactivities, we choose yeast, S. cerevisiae, and used whole genome DNA chips and ***microarray*** technique to examine transcriptional response to coal tar. Although yeast cells are resistant to coal tar, such a treatment causes significant physiol. changes that affect the initial growth. We purified total RNA from treated and control samples. ***Poly*** (***A***)+ mRNAs were converted to cDNA in the presence of fluorescent nucleotides. DNA chips were then hybridized with mixt. of differentially labeled cDNAs. The intensities of fluorescent signals bound to different genes represent the relative abundance of mRNAs and any changes reflect the changes in response to coal tar in the medium. Our anal. of six ***microarray*** data has revealed consistent changes of a fraction of the yeast genome in response to coal tar. We are currently focusing on interpretation of the results.

L12 ANSWER 79 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:176346 CAPLUS <<LOGINID::20061115>>
DN 134:291423
TI Genetic events associated with arsenic-induced malignant transformation: applications of cDNA ***microarray*** technology
AU Chen, Hua; Liu, Jie; Merrick, Bruce A.; Waalkes, Michael P.
CS Laboratory of Comparative Carcinogenesis, NIEHS, Research Triangle Park, NC, 27709, USA
SO Molecular Carcinogenesis (2001), 30(2), 79-87 CODEN: MOCAE8; ISSN: 0899-1987
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Arsenic is a human carcinogen. Our recent work showed that chronic (> 18 wk), low-level (125-500 nM) arsenite exposure induces malignant transformation in normal rat liver cell line TRL 1215. In these arsenic-transformed cells, the cellular S-adenosylmethionine pool was depleted from arsenic metab., resulting in global DNA hypomethylation. DNA methylation status in turn may affect the expression of a variety of genes. This study examd. the aberrant gene expression assocd. with arsenic-induced transformation with the use of Atlas Rat cDNA Expression ***microarrays*** . ***Poly*** (***A*** +) RNA was prepd. from arsenic-transformed cells and passage-matched control cells, and 32P-labeled cDNA probes were synthesized with Clontech Rat cDNA Synthesis primers and moloney murine leukemia virus reverse transcriptase. The hybrid intensity was analyzed with AtlasImage software and normalized with the sum of the four housekeeping genes. Four hybridizations from sep. cell prepns. were performed, and mean and SEM for the expression of each gene were calcd. for statistical anal. Among the 588 genes, approx. 80 genes (.apprx.13%) were aberrantly expressed. These included genes involved in cell-cycle regulation, signal transduction, stress response, apoptosis, cytokine prodn. and growth-factor and hormone-receptor prodn. and various oncogenes. These initial gene expression analyses for the first time showed potentially important aberrant gene expression patterns assocd. with arsenic-induced malignant transformation and set the stage for numerous further studies.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 80 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:159103 CAPLUS <<LOGINID::20061115>>
DN 135:299169
TI Isolation of Escherichia coli mRNA and Comparison of Expression Using mRNA and Total RNA on DNA ***Microarrays***
AU Wendisch, Volker F.; Zimmer, Daniel P.; Khodursky, Arkady; Peter, Brian; Cozzarelli, Nicholas; Kustu, Sydney
CS Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA
SO Analytical Biochemistry (2001), 290(2), 205-213 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
AB Bacterial mRNA (mRNA) is not coherently polyadenylated, whereas mRNA of Eukarya can be sepd. from stable RNAs by virtue of polyadenylated 3'-termini. We have developed a method to isolate Escherichia coli mRNA by polyadenylating it in crude cell exts. with E. coli ***poly*** (***A***) polymerase I and purifying it by oligo(dT) chromatog. Differences in lacZRNA levels were similar with purified mRNA and total RNA in dot blot hydridizations for cultures grown with or without gratuitous induction of the lactose operon. More broadly, changes in gene expression upon induction were similar when cDNAs primed from mRNA or total RNA with random hexanucleotides were hydridized to DNA ***microarrays*** for the E. coli genome. Comparable signal intensities were obtained with only 1% as much oligo(dT)-purified mRNA as total RNA, and hence in vitro ***poly*** (***A***) tailing appears to be selective for mRNA. These and addnl. studies of genome-wide expression with DNA ***microarrays*** provide evidence that in vitro ***poly*** (***A***) tailing works universally for E. coli mRNAs. (c) 2001 Academic Press.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 81 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:148599 CAPLUS <<LOGINID::20061115>>

DN 135:135780
TI Selective alterations in glutamate and GABA receptor subunit mRNA expression in dysplastic neurons and giant cells of cortical tubers
AU White, Ricarda; Hua, Yue; Scheithauer, Bernd; Lynch, David R.; Henske, Elizabeth Petri; Crino, Peter B.
CS PENN Epilepsy Center and Department of Neurology, University of Pennsylvania School of Medicine, Philadelphia, PA, 19104, USA
SO Annals of Neurology (2001), 49(1), 67-78 CODEN: ANNED3; ISSN: 0364-5134
PB Wiley-Liss, Inc.
DT Journal
LA English
AB The mol. pharmacol. basis of epileptogenesis in cortical tubers in the tuberous sclerosis complex is unknown. Altered transcription of genes encoding glutamatergic and .gamma.-aminobutyric acid (GABA)-ergic receptors and uptake sites may contribute to seizure initiation and may occur selectively in dysplastic neurons and giant cells. ***Arrays*** contg. GABA A (GABAAR), GluR, NMDA receptor (NR) subunits, GAD65, the vesicular GABA transporter (VGAT), and the neuronal glutamate transporter (EAAC1) cDNAs were probed with amplified ***poly*** (***A***) mRNA from tubers or normal neocortex to identify changes in gene expression. Increased levels of EAAC1, and NR2B and 2D subunit mRNAs and diminished levels of GAD65, VGAT, GluR1, and GABAAR .alpha.1 and .alpha.2 were obsd. in tubers. Ligand-binding expts. in frozen tuber homogenates demonstrated an increase in functional NR2B-contg. receptors. ***Arrays*** were then probed with ***poly*** (***A***) mRNA from single, microdissected dysplastic neurons, giant cells, or normal neurons (n = 30 each). Enhanced expression of GluR 3, 4, and 6 and NR2B and 2C subunit mRNAs was noted in the dysplastic neurons, whereas only the NR2D mRNA was upregulated in giant cells. GABAAR .alpha.1 and .alpha.2 mRNA levels were reduced in both dysplastic neurons and giant cells compared to control neurons. Differential expression of GluR, NR, and GABAAR mRNAs in tubers reflects cell-specific changes in gene transcription that argue for a distinct mol. phenotype of dysplastic neurons and giant cells and suggests that dysplastic neurons and giant cells make differential contributions to epileptogenesis in the tuberous sclerosis complex.
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 82 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:78405 CAPLUS <<LOGINID::20061115>>
DN 134:126778
TI Even length proportional amplification of nucleic acids
IN Lockhart, David; Lai, Chao-Qiang; Gunderson, Kevin
PA Affymetrix, Inc., USA
SO PCT Int. Appl., 50 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2001007464 A1 20010201 WO 2000-US19841 20000721 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6495320 B1 20021217 US 1999-358664 19990721
PRAI US 1999-358664 A 19990721
AB The present invention addresses the issue of amplifying of DNA or RNA in an unbiased fashion, thus providing the accurate detn. of gene expression in even a single cell or a small amt. of tissue. Even length proportional amplification of nucleic acids can increase the amt. of nucleic acids while preserving the relative abundance of the individual nucleic acid species, or portions thereof, in the original sample. The cDNA target that is synthesized from mRNA is randomly digested into equal or roughly equal length fragments; then an adapter is attached at both ends of these fragments, and subsequently the fragments amplified by PCR. Random digestion into equal length fragments facilitates unbiased PCR amplification of the original mRNA population, and is achieved using 1,10-phenanthroline-copper as a cutter. An even length proportionally amplified nucleic acid prepn. may be analyzed in a gene expression monitoring system, preferably involving a nucleic acid probe ***array*** .
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 83 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:60786 CAPLUS <<LOGINID::20061115>>
DN 135:103294
TI Inactivation of DNA mismatch repair by increased expression of yeast MLH1
AU Shcherbakova, Polina V.; Hall, Mark C.; Lewis, Marc S.; Bennett, Samuel E.; Martin, Karla J.; Bushel, Pierre R.; Afshari, Cynthia A.; Kunkel, Thomas A.
CS Laboratories of Molecular Genetics, National Institute of Environmental Health Sciences, Research Triangle Park, NC, 27709, USA
SO Molecular and Cellular Biology (2001), 21(3), 940-951 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Inactivation of DNA mismatch repair by mutation or by transcriptional silencing of the MLH1 gene results in genome instability and cancer predisposition. We recently found that an elevated spontaneous mutation rate can also result from increased expression of yeast MLH1. Here we investigate the mechanism of this mutator effect. Hybridization of ***poly*** (***A***)+ mRNA to DNA ***microarrays*** contg. 96.4% of yeast open reading frames revealed that MLH1 overexpression did not induce changes in expression of other genes involved in DNA replication or repair. MLH1 overexpression strongly enhanced spontaneous mutagenesis in yeast strains with defects in the 3' .fwdarw. 5' exonuclease activity of replicative DNA polymerases .delta. and .epsilon. but did not enhance the mutation rate in strains with deletions of MSH2, MLH1, or PMS1. This suggests that overexpression of MLH1 inactivates mismatch repair of replication errors. Overexpression of the PMS1 gene alone caused a moderate increase in the mutation rate and strongly suppressed the mutator effect caused by MLH1 overexpression. The mutator effect was also reduced by a missense mutation in the MLH1 gene that disrupted Mlh1p-Pms1p interaction. Anal. ultracentrifugation expts. showed that purified Mlh1p forms a

homodimer in soln., albeit with a Kd of 3.14 .mu.M, 36-fold higher than that for Mlh1p-Pms1p heterodimerization. These observations suggest that the mismatch repair defect in cells overexpressing MLH1 results from an imbalance in the levels of Mlh1p and Pms1p and that this imbalance might lead to formation of nonfunctional mismatch repair complexes contg. Mlh1p homodimers.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 84 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:52408 CAPLUS <<LOGINID::20061115>>
DN 135:252478
TI Cloning of a novel gene associated with human nasopharyngeal carcinoma
AU He, Zhiwei; Xie, Lu; Xu, Liangguo; Lan, Ke; Liu, Weidong; Zhang, Ling; Ren, Caiping; Shi, Jianling; Zhou, Wen; Yao, Kaitai
CS Key Laboratory of Carcinogenesis of Chinese Ministry of Health, Cancer Research Institute of Hunan Medical University, Changsha, 410078, Peop. Rep. China
SO Chinese Science Bulletin (2000), 45(24), 2267-2272 CODEN: CSBUEF; ISSN: 1001-6538
PB Science in China Press
DT Journal
LA English
AB One EST N27741 with high expression in normal adult nasopharynx tissues but low expression in adult poorly differentiated squamous nasopharyngeal carcinoma has been selected out by the high-d. cDNA ***array*** expression profiling technique. The differential expression has been confirmed by RT-PCR. One novel gene of 1096 bp has been cloned based on this EST. Bioinformatics anal. found that the new gene sequence contains a whole reading frame encoding 256 amino acids. There is a stop codon TAA in front of the 5' end start codon, and a tailing signal AATAAA and ***poly*** ***A*** tail at the 3' end. There is no homologous known gene found after searching by blasting this sequence to non-redundancy nucleotide database. Therefore it is considered a novel gene related to nasopharyngeal carcinoma.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 85 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:39843 CAPLUS <<LOGINID::20061115>>
DN 135:132868
TI Quantitative Assessment of DNA ***Microarrays*** - Comparison with Northern Blot Analyses
AU Taniguchi, Masaru; Miura, Katsuyuki; Iwao, Hiroshi; Yamanaka, Shinya
CS Department of Pharmacology, Osaka City University Medical School, Osaka, 545-8585, Japan
SO Genomics (2001), 71(1), 34-39 CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB DNA ***microarray*** is a powerful technol. that provides the expression profile of thousands of genes. However, less attention has been paid to its quant. aspect. In this study, we constructed a small-scale DNA ***microarray*** that contains 84 genes and characterized its quant. aspect. Analyses with this ***microarray*** showed that 17 genes were induced, whereas 8 genes were suppressed at least twofold during the differentiation of mouse embryonic stem cells. When repeated with the same combination of fluorescent dyes for probe labeling, the ***microarray*** produced consistent data (correlation coeff. = 0.991). In contrast, data were less consistent when repeated with the reverse combination of dyes (correlation coeff. = 0.945). The effect of dye combination was particularly evident in several genes. Total RNA (15 .mu.g) and ***poly*** (***A***) RNA (0.5 .mu.g) showed comparable sensitivity and produced essentially identical data (correlation coeff. = 0.983). The sensitivity of the DNA ***microarrays*** was slightly inferior to that of Northern blot analyses. In most genes, data obtained with the two methods were consistent. However, in 4 of 46 genes compared, DNA ***microarrays*** failed to detect the expression changes that were revealed by Northern blot. These data demonstrated that DNA ***microarrays*** provide quant. data comparable to Northern blot in general, but a few issues must be considered when analyzing data. (c) 2001 Academic Press.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 86 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:30496 CAPLUS <<LOGINID::20061115>>
DN 135:103218
TI The Dstpk61 locus of Drosophila produces multiple transcripts and protein isoforms, suggesting it is involved in multiple signalling pathways
AU Clyde, D.; Bownes, M.
CS Institute of Cell and Molecular Biology, The University of Edinburgh, Edinburgh, EH9 3JR, UK
SO Journal of Endocrinology (2000), 167(3), 391-401 CODEN: JOENAK; ISSN: 0022-0795
PB Society for Endocrinology
DT Journal
LA English
AB The Drosophila gene Dstpk61 encodes a serine threonine protein kinase homologous to human phosphoinositide-dependent protein kinase (PDK1), and also has homologues in S. cerevisiae, S. pombe, C. elegans, A. thaliana, mouse, and sheep. Where its function has been investigated, this kinase is thought to be involved in regulating cell growth and survival in response to extracellular signals such as insulin and growth factors. In Drosophila it produces multiple transcripts, some of which appear to be sex-specific. In addn. to the five Dstpk61 cDNAs we have described previously we report the existence of a further 18 expressed sequence tag (EST) cDNAs, three of which we have fully sequenced. We conclude that Dstpk61 is a complex locus that utilizes a combination of alternative promoters, alternative splice sites and alternative ***poly*** - ***adenylation*** sites to produce a vast ***array*** of different transcripts. These cDNAs encode at least four different DSTPK61 protein isoforms with variant N-termini. In this paper, we discuss the possible functions of the distinct Dstpk61 transcripts and how they might be differentially regulated. We also discuss the roles that DSTPK61 protein isoforms might play in relation to the protein domains they contain and their potential targets in the cell. Finally, we report the putative structure of the human PDK1 gene based on computer comparisons of available mRNA and genomic sequences. The value of using sequence data from other species for exptl. design in mammalian systems is discussed.

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 87 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:20424 CAPLUS <<LOGINID::20061115>>
DN 135:103909
TI Identifying mRNA subsets in messenger ribonucleoprotein complexes by using cDNA ***arrays***
AU Tenenbaum, Scott A.; Carson, Craig C.; Lager, Patrick J.; Keene, Jack D.
CS Department of Microbiology, Duke University Medical Center, Durham, NC, 27710, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(26), 14085-14090 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Genomic ***array*** technologies provide a means for profiling global changes in gene expression under a variety of conditions. However, it has been difficult to assess whether transcriptional or posttranscriptional regulation is responsible for these changes. Addnl., fluctuations in gene expression in a single cell type within a complex tissue like a tumor may be masked by overlapping profiles of all cell types in the population. In this paper, we describe the use of cDNA ***arrays*** to identify subsets of mRNAs contained in endogenous messenger ribonucleoprotein complexes (mRNPs) that are cell type specific. We identified mRNA subsets from P19 embryonal carcinoma stem cells by using mRNA-binding proteins HuB, eIF-4E, and PABP that are known to play a role in translation. The mRNA profiles assocd. with each of these mRNPs were unique and represented gene clusters that differed from total cellular RNA. Addnl., the compn. of mRNAs detected in HuB-mRNP complexes changed dramatically after induction of neuronal differentiation with retinoic acid. We suggest that the assocn. of structurally related mRNAs into mRNP complexes is dynamic and may help regulate posttranscriptional events such as mRNA turnover and translation. Recovering proteins specifically assocd. with mRNP complexes to identify and profile endogenously clustered mRNAs should provide insight into structural and functional relationships among gene transcripts and/or their protein products. We have termed this approach to functional genomics ribonomics and suggest that it will provide a useful paradigm for organizing genomic information in a biol. relevant manner.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 88 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:798948 CAPLUS <<LOGINID::20061115>>
DN 134:96068
TI Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis
AU Simmen, Martin W.; Bird, Adrian
CS Institute of Cell and Molecular Biology, University of Edinburgh, Edinburgh, EH9 3JR, UK
SO Molecular Biology and Evolution (2000), 17(11), 1685-1694 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB A systematic search of 1 Mb of genomic sequences from the sea squirt, Ciona intestinalis, revealed the presence of 6 families of transposable elements. The Cigr-1 retrotransposon contains identical 245-bp long terminal repeats (LTRs) and a 3630-bp open reading frame (ORF) encoding translation products in the same order as the domains characteristic of gypsy/Ty3-type LTR retrotransposons. The closest homologs of the reverse transcriptase domain were in gypsy elements from Drosophila and the sushi element from the pufferfish. However, the capsid-nucleocapsid region shows the clearest homol. to an echinoderm element, Tgr1. Database searches also indicated two classes of non-LTR retrotransposon, named Cili-1 and Cili-2. The Cili-1 sequences show matches to regions of the ORF2 product of mammalian L1 elements. The Cili-2 sequences possess similarity to the RNaseH domain of Lian-Aa1, a mosquito non-LTR retrotransposon. The most abundant element was a short interspersed nucleotide element named Cics-1 with a copy no. estd. at 40,000. Cics-1 consists of 2 conserved domains sepd. by an A-rich stretch. The 172-bp 5' domain is related to tRNA sequences, whereas the 110-bp 3' domain is unique. Cics-1 is unusual, not just in its modular structure, but also in its lack of a 3' ***poly*** (***A***) tail or direct flanking repeats. A second abundant element, Cimi-1, has an A+T-rich 193-bp consensus sequence and 30-bp terminal inverted repeats (TIRs) and is usually flanked by A+T-rich 2-4-bp putative target site duplications-characteristics of miniature inverted-repeat transposable elements found in plants and insects. A single 2444-bp foldback element was found, possessing long TIRs contg. an A+T-rich internal domain, an ***array*** of subrepeats, and a flanking domain at the TIR ends; this is the first example of a chordate foldback element. This study provides the first systematic characterization of the families of transposable elements in a lower chordate.
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 89 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:797648 CAPLUS <<LOGINID::20061115>>
TI Xanthene dye aggregation on polypeptide electrolytes.
AU Vullev, Valentine Ivanov; Jones, Guilford, II; Velev, Pavel
CS Department of Chemistry and Center for Photonics, Boston University, Boston, MA, 02215, USA
SO Abstracts of Papers, 220th ACS National Meeting, Washington, DC, United States, August 20-24, 2000 (2000) PHYS-473 CODEN: 69FZC3
PB American Chemical Society
DT Journal; Meeting Abstract
LA English
AB The interest in chromophore aggregates has increased in the recent years because of their relation to the natural light-harvesting systems. Through the progress of the studies on artificial photosynthesis, it has been detd. that some peptide polyelectrolytes can serve as templates for unique polychromophoric aggregate formation. This particular work emphasizes on xanthene deriv. aggregation on charged ***poly*** - ***a*** -amino acids. It is proposed that the chromophores are arranged in tubular ***arrays*** around helical templates. The structural parameters and the binding consts. were extd. from UV/Visible emission, absorption and CD data. Laser flash photolysis was utilized to observe the photokinetics of reactions with external agents. Since similar polychromophoric structures are obsd. in some photosynthetic organisms, this investigation represents an important step in the design of artificial light-harvesting systems.

L12 ANSWER 90 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:759895 CAPLUS <<LOGINID::20061115>>
DN 134:28172
TI The expression of adipogenic genes is decreased in obesity and diabetes mellitus
AU Nadler, Samuel T.; Stoehr, Jonathan P.; Schueler, Kathryn L.; Tanimoto, Gene; Yandell, Brian S.; Attie, Alan D.
CS Department of Biochemistry, University of Wisconsin, Madison, WI, 53706, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(21), 11371-11376 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Obesity is strongly correlated with type 2 diabetes mellitus, a common disorder of glucose and lipid metab. Although adipocytes are crit. in obesity, their role in diabetes has only recently been appreciated. The authors conducted studies by using DNA ***microarrays*** to identify differences in gene expression in adipose tissue from lean, obese, and obese-diabetic mice. The expression level of over 11,000 transcripts was analyzed, and 214 transcripts showed significant differences between lean and obese mice. Surprisingly, the expression of genes normally assocd. with adipocyte differentiation were down-regulated in obesity. Not all obese individuals will become diabetic; many remain normoglycemic despite profound obesity. Understanding the transition to obesity with concomitant diabetes will provide important clues to the pathogenesis of type 2 diabetes. Therefore, the authors examd. the levels of gene expression in adipose tissue from five groups of obese mice with varying degrees of hyperglycemia, and the authors identified 88 genes whose expression strongly correlated with diabetes severity. This group included many genes that are known to be involved in signal transduction and energy metab. as well as genes not previously examd. in the context of diabetes. The authors' data show that a decrease in expression of genes normally involved in adipogenesis is assocd. with obesity, and the authors further identify genes important for subsequent development of type 2 diabetes mellitus.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 91 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:688402 CAPLUS <<LOGINID::20061115>>
DN 133:262259
TI Oligonucleotides with fixed and combinatorial domains and their use in DNA ***arrays*** and hybridization methods
IN Cullen, Paul; Seedorf, Udo; Lorkowski, Stefan
PA Germany
SO PCT Int. Appl., 19 pp. CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2000056921 A2 20000928 WO 2000-EP2492 20000321 WO 2000056921 A3 20020314 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG DE 19945765 A1 20001005 DE 1999-19945765 19990924 EP 1208224 A2 20020529 EP 2000-920528 20000321 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL
PRAI DE 1999-19912983 A 19990322 DE 1999-19945765 A 19990924 WO 2000-EP2492 W 20000321
AB Oligonucleotides with a subfragment comprising a fixed sequence adjacent a subfragment with random sequence is disclosed. This oligonucleotide may be immobilized, e.g., on gold-coated glass, polystyrene, or latex. The (immobilized) oligonucleotides may be used in hybridization assays. Thus, oligonucleotides comprising oligo(T) and a random nonamer may be immobilized to form a DNA ***array*** and used to analyze ***poly*** (***A***)-contg. mRNA. Alternative choices for the fixed sequence are, e.g., a Kozak sequence, a plasmid sequence, a restriction nuclease recognition site, and a polyadenylation signal.

L12 ANSWER 92 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:645291 CAPLUS <<LOGINID::20061115>>
DN 134:348755
TI Partial genome scale analysis of gene expression in human adipose tissue using DNA ***array***
AU Gabrielsson, Britt L.; Carlsson, Bjorn; Carlsson, Lena M. S.
CS Research Centre for Endocrinology & Metabolism, Goteborg University, Goteborg, S-41345, Swed.
SO Obesity Research (2000), 8(5), 374-384 CODEN: OBREFR; ISSN: 1071-7323
PB North American Association for the Study of Obesity
DT Journal
LA English
AB Objective: Large scale anal. of gene expression in adipose tissue provides a basis for the identification of novel candidate genes involved in the pathophysiol. of obesity. Our goal was to explore gene expression in human adipose tissue at a partial genome scale using DNA ***array*** . Research Methods and Procedures: Labeled cDNA, derived from human adipose tissue ***poly*** (***A*** +) RNA, was hybridized to a DNA ***array*** contg. over 18,000 human expressed sequence-tagged (EST) clones. The results were analyzed by database searches. Results: Homol. searches of the 300 EST clones with highest hybridization signals revealed that 145 contained DNA sequences identical to known genes and 79 could be linked to UniGene clusters. Of the 145 identified genes, 136 were nonredundant and subsequently characterized with respect to function and chromosomal localization by searching MEDLINE, UniGene, GeneMap, OMIM, SWISS-PROT, the Genome Database, and the Location Data Base. The identified genes were grouped according to their putative functions; cell/organism defense (9.6%), cell division (5.1%), cell signaling/communication (19.8%), cell structure/motility (12.5%), gene/protein expression (16.9%), metab. (16.2%), and unclassified (19.8%). Less than 50% of these genes have previously been reported to be expressed in adipose tissue. The chromosomal localization of 268 genes strongly expressed in adipose tissue showed that their relative abundance was significantly increased on chromosomes 11, 19, and 22 compared to the expected distribution of the same no. of random genes. Discussion: Our study resulted in the

identification of numerous genes previously not reported to be expressed in adipose tissue. These results suggest that DNA ***array*** is a powerful tool in the search for novel regulatory pathways within adipose tissue on a scale that is not possible using conventional methods.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 93 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:603871 CAPLUS <<LOGINID::20061115>>
DN 133:318457
TI Identification of a possible association between carbon tetrachloride-induced hepatotoxicity and interleukin-8 expression
AU Holden, Peter R.; James, Neil H.; Brooks, A. Nigel; Roberts, Ruth A.; Kimber, Ian; Pennie, William D.
CS Zeneca Central Toxicology Laboratory, Macclesfield, SK10 4TJ, UK
SO Journal of Biochemical and Molecular Toxicology (2000), 14(5), 283-290 CODEN: JBMTFQ; ISSN: 1095-6670
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB Hepatotoxicants can elicit liver damage by various mechanisms that can result in cell necrosis and death. The changes induced by these compds. can vary from gross alterations in DNA repair mechanisms, protein synthesis, and apoptosis, to more discrete changes in oxidative damage and lipid peroxidn. However, little is known of the changes in gene expression that are fundamental to the mechanisms of hepatotoxicity. The authors have used DNA ***microarray*** technol. to identify gene transcription assocd. with the toxicity caused by the hepatotoxicant carbon tetrachloride. Labeled ***poly*** ***A*** + RNA from cultured human hepatoma cells (HepG2) exposed to carbon tetrachloride for 8 h was hybridized to a human ***microarray*** filter. The authors found that 47 different genes were either upregulated or down-regulated more than 2-fold by the hepatotoxicant compared with DMF, a chem. that does not cause liver cell damage. The proinflammatory cytokine interleukin-8 (IL-8) was upregulated over 7-fold compared with control on the ***array*** , and this was subsequently confirmed at 1 h and 8 h by Northern blot analyses. The authors also found that carbon tetrachloride caused a time-dependent increase in interleukin-8 protein release in HepG2 cells, which was parallelled by a decrease in cell viability. These data demonstrate that carbon tetrachloride causes a rapid increase in IL-8 mRNA expression in HepG2 cells and that this increase correlates with a later and significant increase in the levels of interleukin-8 protein. These results illustrate the potential of ***microarray*** technol. in the identification of novel gene changes assocd. with toxic processes.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 94 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:598473 CAPLUS <<LOGINID::20061115>>
DN 134:321332
TI Reproducibility of alternative probe synthesis approaches for gene expression profiling with ***arrays***
AU Vernon, Suzanne D.; Unger, Elizabeth R.; Rajeevan, Mangalathu; Dimulescu, Irina M.; Nisenbaum, Rosane; Campbell, Catherine E.
CS Centers for Disease Control and Prevention, Department of Health and Human Services, United States Public Health Service, Atlanta, Georgia
SO Journal of Molecular Diagnostics (2000), 2(3), 124-127 CODEN: JMDIFP; ISSN: 1525-1578
PB Association for Molecular Pathology
DT Journal
LA English
AB Before gene expression profiling with ***microarray*** technol. can be transferred to the diagnostic setting, we must have alternative approaches for synthesizing probe from limited RNA samples, and we must understand the limits of reproducibility in interpreting gene expression results. The current gold std. of probes for use with both ***microarrays*** and high-d. filter ***arrays*** are synthesized from 1 .mu.g of purified ***poly*** (***A***)+ RNA. We evaluated two approaches for synthesizing cDNA probes from total RNA with subsequent hybridization to high-d. filter ***arrays*** : 1) reverse transcription (RT) of 5 .mu.g total RNA and 2) RT-polymerase chain reaction (RT-PCR) of 1 .mu.g total RNA, using the SMART system. The reproducibility of these two approaches was compared to the current gold std. All three methods were highly reproducible. Triplicate expts. resulted in the following concordance correlation coeffs. to evaluate reproducibility: 0.88 for the gold std., 0.86 for cDNA probe synthesized by RT from total RNA, and 0.96 for the SMART cDNA probe synthesized from total RNA. We also compared the expression profile of 588 genes for the total RNA methods to that obtained with the gold std. Of 150 pos. genes detected by the gold std., 97 (65%) were detected by cDNA probe synthesized by RT of total RNA, and 122 (81%) were detected by the SMART cDNA probe. We conclude that SMART cDNA probe produces highly reproducible results and yields gene expression profiles that represent the majority of transcripts detected with the gold std.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 95 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:568476 CAPLUS <<LOGINID::20061115>>
DN 133:172991
TI Hybridization signal enhancement involving nucleic acid homopolymers and multiple homopolymer-complementary reporter probes
IN Dellinger, Douglas J.; Dahm, Sueann C.; Ilsley, Diane D.; Ach, Robert A.; Troll, Mark A.
PA Agilent Technologies Inc., USA
SO U.S., 18 pp., Cont.-in-part of U.S. 5,853,993. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 6103474 A 20000815 US 1998-183619 19981030 US 5853993 A 19981229 US 1996-735381 19961021 US 6110682 A 20000829 US 1998-201674 19981130
PRAI US 1996-735381 A2 19961021
AB A signal amplification method for detecting a target nucleic acid analyte having a homopolymeric region and a target sequence includes steps of: contacting an analyte under hybridizing conditions with a multiplicity of reporter probes, each reporter probe including a signal region and an oligonucleotide sequence which is complementary to and capable of forming a

stable hybrid with the analyte homopolymeric region to form an analyte:reporter probe hybrid; and forming an analyte:capture probe hybrid by contacting the analyte target sequence with a capture probe under hybridizing conditions. The analyte:reporter probe hybrid may formed prior to contacting the analyte target sequence with the capture probe, so the result of contacting the analyte target sequence with the capture probe results in formation of an analyte:reporter probe:capture probe complex. The analyte:capture probe hybrid may be immobilized on a solid generally planar surface in an ***array*** format. Multiple reporter probes may form triple helix structures for further signal enhancement. Multiply-labeled hairpin reporter probes may be employed according to the invention. Also, a kit for carrying out the invention includes one or more capture probes immobilized on a surface, reporter probes each having a signal region and a sequence for binding analyte homopolymer regions, and, optionally, reagents for addn. of homopolymer regions to nucleic acid analytes and for carrying out the hybridization reaction.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 96 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:314871 CAPLUS <<LOGINID::20061115>>
DN 132:330583
TI Nucleic acid analysis using sequence-targeted tandem stacking hybridization of pre-annealed duplex probes
IN Beattie, Kenneth Loren; Maldonado Rodriguez, Rogelio
PA USA
SO PCT Int. Appl., 129 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2000026412 A1 20000511 WO 1999-US25693 19991102 W: CA, JP, MX RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1998-106655P P 19981102
AB The disclosed invention provides a novel method for analyzing genomic DNA and expressed sequences, using auxiliary oligonucleotides preannealed to the single-stranded target nucleic acid to form a partially duplex target mol., which offers several advantages in the anal. of nucleic acid sequences by hybridization to genosensor ***arrays*** or "DNA chips". Also provided is a method for directly analyzing and comparing patterns of gene expression at the level of transcription in different cellular samples.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 97 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:302873 CAPLUS <<LOGINID::20061115>>
DN 133:116659
TI Discovery of molecular and catalytic diversity among human diphosphoinositol-polyphosphate phosphohydrolases. An expanding NUDT family
AU Caffrey, James J.; Safrany, Stephen T.; Yang, Xiaonian; Shears, Stephen B.
CS Inositide Signaling Group, NIEHS, National Institutes of Health, Research Triangle Park, NC, 27709, USA
SO Journal of Biological Chemistry (2000), 275(17), 12730-12736 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The turnover of the "high energy" diphosphoinositol polyphosphates by Ca2+ - and cyclic nucleotide-modulated enzymes is considered a regulatory, mol. switching activity. Target processes may include intracellular trafficking. Following our earlier identification of a prototype human diphosphoinositol-polyphosphate phosphohydrolase (hDIPP1), we now describe new 21-kDa human isoforms, hDIPP2.alpha. and hDIPP2.beta., distinguished from each other solely by hDIPP2.beta. possessing one addnl. amino acid (Gln86). Candidate DIPP2.alpha. and DIPP2.beta. homologs in rat and mouse were also identified. The rank order for catalytic activity is hDIPP1 > hDIPP2.alpha. > hDIPP2.beta.. Differential expression of hDIPP isoforms may provide flexibility in response times of the mol. switches. The 76% identity between hDIPP1 and the hDIPP2s includes conservation of an emerging signature sequence, namely, a Nudt (MutT) motif with a GX2GX6G carboxy extension. Northern and Western analyses indicate expression of hDIPP2s is broad but atypically controlled; these proteins are translated from multiple mRNAs that differ in the length of the 3'-untranslated region because of utilization of an ***array*** of alternative (canonical and noncanonical) polyadenylation signals. Thus, cells can recruit sophisticated mol. processes to regulate diphosphoinositol polyphosphate turnover.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 98 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:297676 CAPLUS <<LOGINID::20061115>>
DN 133:133044
TI Gene expression profiles of the collecting duct in the mouse renal inner medulla
AU Takenaka, Masaru; Imai, Enyu; Nagasawa, Yasuyuki; Matsuoka, Yasuko; Moriyama, Toshiki; Kaneko, Tetsuya; Hori, Masatsugu; Kawamoto, Shoko; Okubo, Kousaku
CS Department of Internal Medicine and Therapeutics, Osaka University Graduate School of Medicine, School of Health and Sport Sciences, Osaka University, Osaka, Japan
SO Kidney International (2000), 57(1), 19-24 CODEN: KDYIA5; ISSN: 0085-2538
PB Blackwell Science, Inc.
DT Journal
LA English
AB Background: Gene expression profiles, constructed from 1000 to 2000 cloned cDNA sequences, depict their relative abundance of expression in a tissue. Establishing such a profile for mouse inner renal medullary collecting ducts (IMCDs), we compared expression patterns with those in other tissues including proximal tubule. Methods: A nonbiased 3'-end cDNA library was prepd. from microdissected mouse IMCDs. Single-pass sequencing of 2000 randomly selected cDNA clones collected short sequences (approx. length, 250 bp) following ***poly*** (***A***), called gene signatures (GS). Identical sequences were considered a single GS. GS occurrence was quantitated to yield a list of expressed genes indicating their abundance. Results: Among 2000 clones, 1613 types of transcripts were found in IMCDs; 155 were identical or homologous to reported genes. The gene most expressed in IMCDs was .alpha.B-crystallin, a small stress (heat-shock) protein that is also a major structural protein in the ocular lens. According to Northern anal., renal expression of this mRNA was induced by dehydration, presumably via tissue hypertonicity.

However, expression did not change with acute NaCl loading. Also, a new member of the glutathione-S-transferase family was identified by comparing the IMCD expression profile with those of other tissues. Conclusion: With out database of genes expressed in mouse IMCDs, we are devising an IMCD-specific ***microarray*** to study gene-expression responses to various physiol. alterations.
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 99 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:265624 CAPLUS <<LOGINID::20061115>>
DN 133:160329
TI High-fidelity mRNA amplification for gene profiling
AU Wang, Ena; Miller, Lance D.; Ohnmacht, Galen A.; Liu, Edison T.; Marincola, Francesco M.
CS Surgery Branch, Division of Clinical Sciences, National Cancer Institute and the Department of Transfusion Medicine, Clinical Center, National Institutes of Health, Bethesda, MD, USA
SO Nature Biotechnology (2000), 18(4), 457-459 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
AB Gene profiling using cDNA ***microarrays*** is limited by the amt. of RNA available. The authors have devised a procedure that optimizes amplification of low-abundance RNA samples by combining antisense RNA (aRNA) amplification with a template-switching effect. The fidelity of aRNA amplified from 1:10,000 to 1:100,000 of commonly used input RNA was comparable to expression profiles obsd. with conventional ***poly*** (***A***) RNA- or T-RNA-based ***arrays***
.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 100 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:250543 CAPLUS <<LOGINID::20061115>>
DN 134:39574
TI Molecular architecture of bryophyte genes: putative polyadenylation signals in cDNA 3'-ends of the desiccation-tolerant moss Tortula ruralis
AU Wood, Andrew J.; Duff, R. Joel; Zeng, Qin; Oliver, Melvin J.
CS Department of Plant Biology, Southern Illinois University-Carbondale, Carbondale, IL, 62901-6509, USA
SO Bryologist (2000), 103(1), 44-51 CODEN: BRYOAM; ISSN: 0007-2745
PB American Bryological and Lichenological Society
DT Journal
LA English
AB Tortula ruralis is a desiccation-tolerant bryophyte with a novel post-transcriptional gene response to drying and rehydration. To better understand the mol. basis of mRNA stability and selective mRNA translation upon rehydration, 149 T. ruralis cDNAs were selected and analyzed by sequence comparison for the presence of cis-acting elements assocd. with the formation of mRNA 3'-ends. The cDNAs analyzed were 140 expressed sequence tags (ESTs) isolated from desiccated gametophytes (AI304967-AI305106), a calmodulin-like domain protein kinase (U82087), the rehydrins Tr155 (U40818) and Tr288 (U21679), and six previously unreported ESTs isolated from desiccated gametophytes (AI665854-AI665859). The majority of cDNAs contained within the 3' untranslated region a consensus AAUAAA ***poly*** (***A***) signal and a highly conserved far-upstream element (FUE) that was similar to the plant consensus GU-rich sequence. The T. ruralis FUE consensus sequence is WUUUUGUUK (where W = A + U and K = G + U) which we have designated as the UUG-core motif. We have characterized five classes of cDNAs based upon the modular architecture of the ***poly*** (***A***) signal motif. Each cDNA class, with the exception of class V, contained the UUG-core motif. Class I (18% of the total) contained the conserved ***poly*** (***A***) signal sequence 0-30 nucleotides from the ***poly*** (***A***) site. Class II (28% of the total) contained a consensus hexanucleotide 0-30 nucleotides from the ***poly*** (***A***) site. Class III (2% of the total) contained an exact copy of a related ***poly*** (***A***) signal (AAUGAA) more than 30 nucleotides from the ***poly*** (***A***) site. Class IV (20% of the total) contained a consensus hexanucleotide more than 30 nucleotides from the ***poly*** (***A***) site. Class V (32% of the total) contained no known ***poly*** (***A***) signal. Anal. of the relative frequency of sequences between 1 and 60 nucleotides upstream from the ***poly*** (***A***) tail was detd. for each cDNA sequence. Overall, the 60 nucleotide sequence was found to be U-rich and C/G poor with an A-rich region between nucleotides 10 and 30. Putative ***poly*** (***A***) signals are ***arrayed*** within the 3' untranslated region of T. ruralis cDNAs as predicted from the angiosperm model systems, including the absence of a conserved unifying cis-acting motif. To our knowledge, this is the first description of the mol. architecture of ***poly*** (***A***) signals within moss cDNAs.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 101 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:229857 CAPLUS <<LOGINID::20061115>>
DN 133:148328
TI Identification of genes overexpressed in head and neck squamous cell carcinoma using a combination of complementary DNA subtraction and ***microarray*** analysis
AU Villaret, Douglas B.; Wang, Tongtong; Dillon, Davin; Xu, Jiangchun; Sivam, Dhileep; Cheever, Martin A.; Reed, Steven G.
CS Department of Otolaryngology-Head and Neck Surgery, University of Florida, Gainesville, FL, 32610, USA
SO Laryngoscope (2000), 110(3, Pt. 1), 374-381 CODEN: LARYA8; ISSN: 0023-852X
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Unique genes specific for squamous cell carcinoma of the head and neck for eventual development as tumor markers and vaccine candidates were identified in fresh-frozen head and neck squamous cell cancer (HNSCC). A subtractive library was made from two HNSCC and six normal tissues using a polymerase chain reaction (PCR)-based approach. Genes from this library were PCR amplified and placed on a ***microarray*** glass slide. RNA was prepd. or obtained from 16 fresh-frozen HNSCC and 22 normal tissue sources. Fluorescent probes were made from the ***polyA*** + RNA derived from the tumor and normal tissues. The probes were hybridized to the glass slides and excited by a tuneable laser. One hundred seven of the genes showing the highest differential fluorescence value between tumor and normal tissue were identified by sequence anal. Thirteen independent genes were found to be overexpressed in tumor tissues. Of

these, nine were previously known: keratins K6 and K16, laminin-5, plakophilin-1, matrix metalloproteinase-2 (MMP), vascular endothelial growth factor, connexin 26, 14-3-3 sigma, and CaN19. The level of ***polyA*** + RNA of these genes in the tumors was significantly different from the levels in normal tissue. Four previously unidentified genes were also discovered to have increased expression in tumor tissue. Comparing the total tumor group to the normal group, only one of these genes showed significant overexpression. The authors report the identification of nine known genes that are significantly overexpressed in HNSCC as compared to normal tissue using subtractive and ***microarray*** technol. In addn., the authors present four previously unidentified genes that are overexpressed in a subset of tumors. These genes will be developed as tumor markers and vaccine candidates.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 102 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:819564 CAPLUS <<LOGINID::20061115>>
DN 132:47217
TI Multi-sensor ***array*** for electrochemical recognition of nucleotide sequences and methods
IN De Lumley-Woodyear, Thierry; Caruana, Daren J.; Heller, Adam
PA E. Heller & Co., USA
SO PCT Int. Appl., 80 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 9967628 A1 19991229 WO 1999-US14460 19990624 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 9948338 A1 20000110 AU 1999-48338 19990624 EP 1090286 A1 20010411 EP 1999-931928 19990624 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2002518998 T2 20020702 JP 2000-556236 19990624 US 2002081588 A1 20020627 US 2000-746620 20001221
PRAI US 1998-90517P P 19980624 US 1998-93100P P 19980716 US 1999-114919P P 19990105 WO 1999-US14460 W 19990624
AB The invention concerns sensors, sensor ***arrays*** , methods of their prodn. and their usage in the electrochem. detection of nucleic acid sequences for diagnostic purposes. The nucleic acid sensor comprises: an electrode; a redox polymer disposed on the electrode; and an oligonucleotide probe coupled to the redox polymer, wherein the probe optionally comprises DNA, RNA (which can be rRNA); the sensor optionally comprising a catalyst, wherein the catalyst preferably is an enzyme, a thermostable enzyme, a peroxidase, or a soybean peroxidase. ***Arrays*** are comprising a plurality of elec. isolated nucleic acid sensors disposed on a substrate, wherein each nucleic acid sensor comprises a particular oligonucleotide probe, wherein optionally at least two oligonucleotide probes comprise differing diagnostic sequences, and/or one or more of the probes optionally is diagnostic of a cancer, a disease, a pathogen, or a combination thereof.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 103 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:730947 CAPLUS <<LOGINID::20061115>>
DN 132:192482
TI Gene expression profiles in squamous esophageal cancer tissues and adjacent tissues
AU Zhou, Jin; Liu, Zhihua; Wang, Xiuqin; Zhou, Chuannong; Zhao, Jun; Zhang, Rugang; Wu, Min
CS Cancer Institute, Chinese Academy of Medical Science, Beijing, 100021, Peop. Rep. China
SO Zhonghua Yixue Yichuanxue Zazhi (1999), 16(5), 303-306 CODEN: ZYXZER; ISSN: 1003-9406
PB Huaxi Yike Daxue
DT Journal
LA Chinese
AB The authors studied an esophageal cancer-specific expression profile and identified genes that showed altered expression in squamous esophageal cancer tissues and their adjacent almost normal tissues. Some cDNA probes were synthesized from ***polyA*** + RNA of cancer and adjacent almost normal tissues and were differentially hybridized with two identical Atlas human cDNA expression ***arrays*** membranes contg. 588 known genes. Of the 588 genes analyzed, 61 were up-regulated in cancer, including cdc25B, Notchl, MMP, MET; and 22 down-regulated in cancer, including cytokeratin 4, BAD, IL-1 RECEPTOR ANTAGONIST, IL-6. Expression levels of genes that assocd. with the regulation of cell proliferation, apoptosis, differentiation and metastasis altered most. Conclusion: The results provide an esophageal cancer-specific expression profile, showing that complex alterations of gene expression underlie the development of malignant phenotype of esophageal cancer cells. In addn., this line of research can lead to the identification of EC-specific genes which may be helpful for the development of diagnostic and prognostic biomarkers or therapeutic targets. The differential hybridization technique of Atlas Human cDNA expression ***array*** can be a useful method for describing the expression profiles of a tissue of cell interested.

L12 ANSWER 104 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:720972 CAPLUS <<LOGINID::20061115>>
DN 132:45521
TI In the laboratory: A high-density probe ***array*** sample preparation method using 10- to 100-fold fewer cells
AU Mahadevappa, Mamatha; Warrington, Janet A.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Nature Biotechnology (1999), 17(11), 1134-1136 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
AB ***Poly*** (***A***) prepn. methods generally require large amts. of starting material because of sample loss during isolation. In an effort to reduce the amt. of required starting material, we describe a method that eliminates the ***poly*** (***A***) extn. step and uses total RNA as the template in a cDNA reaction. We compare this method with the std. ***poly*** (***A***) RNA method and report results

obtained from hybridizing samples prepd. from 50,000, 100,000, and 200,000 cells. Sample prepn. method begins with total RNA extn. from cells or tissues. Double-stranded cDNA synthesis is followed by in vitro transcription for amplification and labeling of targets. Labeled target is fragmented and hybridized to GeneChip ***arrays*** overnight. After washing and staining, ***arrays*** are scanned. Comparable expression results were obtained from hybridizing samples prepd. by the total RNA and ***poly*** (***A***) RNA methods. The total RNA method requires substantially less starting material to achieve sensitivity similar to that of the ***poly*** (***A***) RNA method. These expts. demonstrate that with limited amts. of starting material (250 pg of tissue, 50,000 cells), we are able to obtain 75-80% of the information obtained with six times as many cells (300,000) or with 100 times as many cells as recommended by the current ***poly*** (***A***) method. Although this method is efficient, it does not solve the problem of measuring expression from one or a few cells; however, it does provide a simple means for prepg. samples from tens of thousands of cells without using PCR.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 105 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:686628 CAPLUS <<LOGINID::20061115>>
DN 131:318541
TI Apparatus for identifying, classifying, or quantifying DNA sequences in a sample without sequencing
IN Rothberg, Jonathan Marc; Deem, Michael W.; Simpson, John W.
PA Curagen Corporation, USA
SO U.S., 110 pp., Cont.-in-part of U.S. 5,871,697. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 5972693 A 19991026 US 1996-663823 19960614 US 5871697 A 19990216 US 1995-547214 19951024 CA 2235860 AA 19970501 CA 1996-2235860 19961024 WO 9715690 A1 19970501 WO 1996-US17159 19961024 W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, FI, GE, HU, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG AU 9674763 A1 19970515 AU 1996-74763 19961024 AU 730830 B2 20010315 EP 866877 A1 19980930 EP 1996-936985 19961024 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2000500647 T2 20000125 JP 1997-516817 19961024 IL 124185 A1 20001206 IL 1996-124185 19961024 US 6141657 A 20001031 US 1997-942406 19971001 US 6231812 B1 20010515 US 1999-322617 19990528 US 6432361 B1 20020813 US 2000-724385 20001128 US 2001007985 A1 20010712 US 2000-751561 20001229 US 6418382 B2 20020709 US 2002058256 A1 20020516 US 2001-757528 20010110 US 6453245 B2 20020917
PRAI US 1995-547214 A2 19951024 US 1996-663823 A 19960614 WO 1996-US17159 W 19961024 US 1997-942406 A1 19971001 US 1999-322617 A1 19990528 US 2000-724385 A1 20001128
AB This invention provides methods, named Quant. Expression Anal. (QEA.RTM.), by which biol. derived DNA sequences in a mixed sample or in an ***arrayed*** single sequence clone can be detd. and classified without sequencing. The methods make use of information on the presence of carefully chosen target subsequences, typically of length from 4 to 8 base pairs, and preferably the length between target subsequences in a sample DNA sequence together with DNA sequence databases contg. lists of sequences likely to be present in the sample to det. a sample sequence. The preferred method uses restriction endonucleases to recognize target subsequences and cut the sample sequence. Then carefully chosen recognition moieties are ligated to the cut fragments, the fragments amplified, and the exptl. observation made. Polymerase chain reaction (PCR) is the preferred method of amplification. Several alternative embodiments are described which capable of increased discrimination and which use Type IIS restriction endonucleases, various capture moieties, or samples of specially synthesized cDNA. Another embodiment of the invention named colony calling (CC) uses information on the presence or absence of carefully chosen target subsequences in a single sequence clone together with DNA sequence databases to det. the clone sequence. Computer implemented methods are provided to analyze the exptl. results and to det. the sample sequences in question and to carefully choose target subsequences in order that expts. yield a max. amt. of information.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 106 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:468500 CAPLUS <<LOGINID::20061115>>
DN 131:85131
TI Solid-phase sample-retaining tips and uses for synthesizing or detecting of biomolecules
IN Garrison, Lori K.; Tabone, John C.; Van Ness, Jeffrey
PA Rapigene, Inc., USA
SO PCT Int. Appl., 72 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 9934214 A1 19990708 WO 1998-US27850 19981230 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CA 2315296 AA 19990708 CA 1998-2315296 19981230 AU 9920989 A1 19990719 AU 1999-20989 19981230 EP 1040352 A1 20001004 EP 1998-965546 19981230 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI BR 9814604 A 20001017 BR 1998-14604 19981230 HU 200100697 A2 20010628 HU 2001-697 19981230 JP 2002500362 T2 20020108 JP 2000-526814 19981230
PRAI US 1997-70290P P 19971231 WO 1998-US27850 W 19981230

AB Solid-phase assays have provided a powerful approach to the anal. of biomols. in medical diagnosis and in basic research. Solid-phase nucleic acid hybridization methods, for example, have been applied to anal. of genetic polymorphisms, diagnosis of genetic disease, cancer diagnosis, detection of viral and microbial pathogens, screening of clones, and ordering of genomic fragments. A new solid-phase sample-retaining tip provides improved procedures for synthesizing or detecting a biomol. These tips can be used to devise sample-retaining assemblies, which in turn, can be combined to form ***arrays*** of solid-phase sample-retaining assemblies useful in automated processes. The tips may be connectable to a spring biased support pin and also contain a chem. layer coating said tip to which a biomol. is bindable.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 107 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:454267 CAPLUS <<LOGINID::20061115>>
DN 131:85124
TI Polymeric ***arrays*** and methods for their use in binding assays
IN Chenchik, Alex; Siebert, Paul
PA Clontech Laboratories, Inc., USA
SO PCT Int. Appl., 35 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 9935289 A1 19990715 WO 1999-US248 19990106 W: AU, CA, JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US 6087102 A 20000711 US 1998-3723 19980107 CA 2312848 AA 19990715 CA 1999-2312848 19990106 AU 9920280 A1 19990726 AU 1999-20280 19990106 AU 743731 B2 20020131 EP 1051513 A1 20001115 EP 1999-900772 19990106 R: DE, FR, GB JP 2002500374 T2 20020108 JP 2000-527670 19990106 US 6287768 B1 20010911 US 2000-269586 20000303 US 6489159 B1 20021203 US 2000-675915 20000929
PRAI US 1998-3723 A 19980107 WO 1999-US248 W 19990106 US 2000-269586 A2 20000303
AB ***Arrays*** of polymeric targets stably assocd. with the surface of a rigid solid support are provided. In the subject ***arrays*** , the polymeric targets are arranged at least according to size. The polymeric targets of the subject ***arrays*** are generally biopolymeric compds., e.g. nucleic acids and proteins, where ribonucleic acids and proteins are the preferred polymeric targets. The subject ***arrays*** find use in a variety of different applications, and are particularly suited for use in high through gene expression anal. applications.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 108 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:277216 CAPLUS <<LOGINID::20061115>>
DN 131:100063
TI Characterization of Xenopus RalB and its involvement in F-actin control during early development
AU Moreau, Jacques; Lebreton, Stephanie; Iouzalen, Nathalie; Mechali, Marcel
CS Laboratoire d'Etude des Mecanismes Moleculaires du Developpement, Institut Jacques Monod, CNRS, Universite Paris VI-VII, Paris, 75251, Fr.
SO Developmental Biology (1999), 209(2), 268-281 CODEN: DEBIAO; ISSN: 0012-1606
PB Academic Press
DT Journal
LA English
AB We describe the characterization and a functional anal. in Xenopus development of RalB, a small G protein. RalB RNA and protein are detectable during oogenesis and early development, but the gene is expressed only weakly in adult tissues. The RalB transcripts are processed by ***poly*** (***A***) extension during oocyte maturation and up to the gastrulation stage. Microinjection of wild-type or mutant RalB RNAs was performed in fertilized eggs to gain insight into the function of RalB during development. During cleavage stages the activated GTP form of RalB specifically induces a cortical reaction that affects the localization of pigment granules. The use of different drugs suggests that this reaction is dependent on the outer cortical actin ***array*** . The relation between F-actin and RalB was shown by confocal anal. Injection of mRNAs encoding the mutated activated form of RalB leads, at dependent doses, to a blocking of gastrulation or defects in closing of neural folding structures. In contrast, the inactivated form blocks only the closing of neural tube. Altogether, these observations suggest that RalB is part of a regulatory pathway that may affect the blastomere cytoskeleton and take part in early development. (c) 1999 Academic Press.
RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 109 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:765634 CAPLUS <<LOGINID::20061115>>
DN 130:137555
TI Cellular gene expression altered by human cytomegalovirus: global monitoring with oligonucleotide ***arrays***
AU Zhu, Hua; Cong, Jian-Ping; Mamtora, Gargi; Gingeras, Thomas; Shenk, Thomas
CS Howard Hughes Medical Institute, Department of Molecular Biology, Princeton University, Princeton, NJ, 08544, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(24), 14470-14475 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Mechanistic insights to viral replication and pathogenesis generally have come from the anal. of viral gene products, either by studying their biochem. activities and interactions individually or by creating mutant viruses and analyzing their phenotype. Now it is possible to identify and catalog the host cell genes whose mRNA levels change in response to a pathogen. We have used DNA ***array*** technol. to monitor the level of .apprxeq.6,600 human mRNAs in uninfected as compared with human cytomegalovirus-infected cells. The level of 258 mRNAs changed by a factor of 4 or more before the onset of viral DNA replication. Several of these mRNAs encode gene products that might play key roles in virus-induced pathogenesis, identifying them as intriguing targets for further study.
RE.CNT 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 110 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:711813 CAPLUS <<LOGINID::20061115>>
DN 130:63469
TI Identification of differentially expressed mRNA in prokaryotic organisms by customized amplification libraries (DECAL): the effect of isoniazid on gene expression in Mycobacterium tuberculosis
AU Alland, David; Kramnik, Igor; Weisbrod, Torin R.; Otsubo, isaA; Cerny, Rosaria; Miller, Lincoln P.; Jacobs, William R.; Bloom, Barry R.
CS Division of Infectious Diseases, Montefiore Medical Center, Bronx, NY, 10467, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(22), 13227-13232 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Understanding the effects of the external environment on bacterial gene expression can provide valuable insights into an ***array*** of cellular mechanisms including pathogenesis, drug resistance, and, in the case of Mycobacterium tuberculosis, latency. Because of the absence of ***poly*** (***A***)+ mRNA in prokaryotic organisms, studies of differential gene expression currently must be performed either with large amts. of total RNA or rely on amplification techniques that can alter the proportional representation of individual mRNA sequences. The authors have developed an approach to study differences in bacterial mRNA expression that enables amplification by the PCR of a complex mixt. of cDNA sequences in a reproducible manner that obviates the confounding effects of selected highly expressed sequences, e.g., rRNA. Differential expression using customized amplification libraries (DECAL) uses a library of amplifiable genomic sequences to convert total cellular RNA into an amplified probe for gene expression screens. DECAL can detect 4-fold differences in the mRNA levels of rare sequences and can be performed on as little as 10 ng of total RNA. DECAL was used to investigate the in vitro effect of the antibiotic isoniazid on M. tuberculosis, and three previously uncharacterized isoniazid-induced genes, iniA, iniB, and iniC, were identified. The iniB gene has homol. to cell wall proteins, and iniA contains a phosphopantetheine attachment site motif suggestive of an acyl carrier protein. The iniA gene is also induced by the antibiotic ethambutol, an agent that inhibits cell wall biosynthesis by a mechanism that is distinct from isoniazid. The DECAL method offers a powerful new tool for the study of differential gene expression.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 111 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:453840 CAPLUS <<LOGINID::20061115>>
DN 129:238569
TI Self-assembled fluorocarbon films for enhanced stiction reduction
AU Srinivasan, Uthara; Houston, Michael R.; Howe, Roger T.; Maboudian, Roya
CS Berkeley Sensor & Actuator Center, University of California, Berkeley, CA, 94720, USA
SO Transducers 97, International Conference on Solid-State Sensors and Actuators, Chicago, June 16-19, 1997 (1997), Volume 2, 1399-1402 Publisher: Institute of Electrical and Electronics Engineers, New York, N. Y. CODEN: 66KBAZ
DT Conference
LA English
AB We have developed a fluorinated self-assembled monolayer (SAM) coating process for stiction redn. in polysilicon MEMS that does not use chlorinated solvents. Using this process, cantilever beams up to 2 mm in length emerge from the final water rinse dry and released. Beam ***arrays*** fabricated from two types of polysilicon were used to characterize in-use stiction. In the first set of structures (***poly*** ***A*** , rms roughness .apprxeq. 12 nm), all beams out to the max. length of 1 mm remained unstuck following actuation, giving an adhesion energy per apparent contact area of less than 2.4 .mu.J/m2. Poly B structures (rms roughness .apprxeq. 3 nm) gave an apparent adhesion energy of 5.2 .mu.J/m2 compared to 23 .mu.J/m2 for the OTS SAM coating. The fluorinated SAMs survive heat treatment in both air and N2 at 400.degree.C for 5 min and are thus compatible with several MEMS packaging processes.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 112 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:273022 CAPLUS <<LOGINID::20061115>>
DN 129:77290
TI Molecular cloning and functional heterologous expression of two alleles encoding (S)-N-methylcoclaurine 3'-hydroxylase (CYP80B1), a new methyl jasmonate-inducible cytochrome P-450-dependent mono-oxygenase of benzylisoquinoline alkaloid biosynthesis
AU Pauli, Hubert H.; Kutchan, Toni M.
CS Laboratorium fur Molekulare Biologie, Universitat Munchen, Munchen, 80333, Germany
SO Plant Journal (1998), 13(6), 793-801 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Alkaloids derived from the tetrahydrobenzylisoquinoline alkaloid (S)-N-methylcoclaurine represent a vast and varied structural ***array*** of physiol. active mols. These compds. range from the dimeric bisbenzylisoquinolines, such as the muscle relaxant (+)-tubocurarine, to the powerful anesthetic opiate morphine, the antimicrobial berberine and the anti-microbial benzo[c]-phenanthridine sanguinarine. The 3'-hydroxylation of (S)-N-methylcoclaurine is a branch point that is the penultimate step in the biosynthesis of the central alkaloidal intermediate (S)-reticuline. This study identified this enzyme as a cytochrome P 450-dependent monooxygenase that has until now eluded attempts at identification using in vitro enzyme assays. Two alleles encoding this new enzyme (S)-N-methylcoclaurine 3'-hydroxylase (CYP80B1) were isolated from a cDNA library prepd. from ***poly*** (***A***)+ RNA isolated from Me jasmonate-induced cell-suspension cultures of the California poppy Eschscholzia californica. Partial clones generated by RT-PCR with cytochrome P 450-specific primers were used as hybridization probes. RNA gel-blot hybridization indicated that the transcripts for CYP80B1 accumulate in response to the addn. of Me jasmonate to the cell culture medium. BOth alleles were functionally expressed in Saccharomyces cerevisiae and in Spodoptera frugiperda Sf9 cells in the presence and absence of the E. californica cytochrome P 450 reductase. The enzyme was found to hydroxylate exclusively (S)-N-methylcoclaurine with a pH optimum of 7.5, temp. optimum of 35.degree.C and a Km of 15 .mu.m. In addn. to the CYP80B1 alleles, another cytochrome P 450 with an inducible transcript (CYP82B1) was isolated and

expressed in the same manner, but was not found to be involved in alkaloid biosynthesis in this plant.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 113 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:173153 CAPLUS <<LOGINID::20061115>>
DN 128:306794
TI Presence and phosphorylation of transcription factors in developing dendrites
AU Crino, Peter; Khodakhah, Kamran; Becker, Kevin; Ginsberg, Stephen; Hemby, Scott; Eberwine, James
CS Departments of Pharmacology, University of Pennsylvania School of Medicine, Philadelphia, PA, 19104, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(5), 2313-2318 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB In screening amplified ***poly*** (***A***) mRNA from hippocampal dendrites and growth cones in culture to det. candidates for local translation, we found that select transcription factor mRNAs were present. We hypothesized that synthesis of transcription factor proteins within dendrites would provide a direct signaling pathway between the distal dendrite and the nucleus resulting in modulation of gene expression important for neuronal differentiation. To evaluate this possibility, radiolabeled amplified antisense RNA was used to probe slot blots of transcription factor cDNAs as well as ***arrayed*** blots of zinc finger transcription factors. The mRNAs encoding the cAMP response element binding protein (CREB), zif 268, and one putative transcription factor were detected. We expanded upon these results showing that CREB protein is present in-dendrites, that translation of CREB mRNA in isolated dendrites is feasible and that CREB protein found in dendrites can interact with the cis-acting cAMP response element DNA sequence by using an in situ Southwestern assay. Further, CREB protein in dendrites is not transported to this site from the cell body because fluorescently tagged CREB microperfused into the soma did not diffuse into the dendrites. In addn., CREB protein microperfused into dendrites was rapidly transported to the nucleus, its likely site of bioactivity. Lastly, by using the isolated dendrite system we show that phosphorylation of Ser-133 on CREB protein can occur in isolated dendrites independent of the nucleus. These data provide a regulatory pathway in which transcription factors synthesized and posttranslationally modified in dendrites directly alter gene expression bypassing the integration of signal transduction pathways that converge on the nucleus.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 114 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1997:450357 CAPLUS <<LOGINID::20061115>>
DN 127:171889
TI Alternative ***poly*** (***A***) site selection in complex transcription units: means to an end?
AU Edwalds-Gilbert, Gretchen; Veraldi, Kristen L.; Milcarek, Christine
CS Dep. Mol. Genetics and Biochemistry and Graduate Program in Immunology, Univ. Pittsburgh Medicine, Pittsburgh, PA, 15261-2072, USA
SO Nucleic Acids Research (1997), 25(13), 2547-2561 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal; General Review
LA English
AB A review with 287 refs. Many genes have been described and characterized which result in alternative polyadenylation site use at the 3'-end of their mRNAs based on the cellular environment. In this survey and summary article 95 genes are discussed in which alternative polyadenylation is a consequence of tandem ***arrays*** of ***poly*** (***A***) signals within a single 3'-untranslated region. An addnl. 31 genes are described in which polyadenylation at a promoter-proximal site competes with a splicing reaction to influence expression of multiple mRNAs. Some have a composite internal/terminal exon which can be differentially processed. Others contain alternative 3'-terminal axons, the first of which can be skipped in some cells. In some cases the mRNAs formed from these three classes of genes are differentially processed from the primary transcript during the cell cycle or in a tissue-specific or developmentally specific pattern. Ig heavy chain genes have composite exons; regulated prodn. of two different Ig mRNAs has been shown to involve B cell stage-specific changes in trans-acting factors involved in formation of the active polyadenylation complex. Changes in the activity of some of these same factors occur during viral infection and take-over of the cellular machinery, suggesting the potential applicability of at least some aspects to the Ig model. The differential expression of a no. of genes that undergo alternative ***poly*** (***A***) site choice or polyadenylation/splicing competition could be regulated at the level of amts. and activities of either generic or tissue-specific polyadenylation factors and/or splicing factors.

L12 ANSWER 115 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1997:434449 CAPLUS <<LOGINID::20061115>>
DN 127:157407
TI Zepp, a LINE-like retrotransposon accumulated in the Chlorella telomeric region
AU Higashiyama, Takanobu; Noutoshi, Yoshiteru; Fujie, Makoto; Yamada, Takashi
CS Faculty Engineering, Hiroshima University, Higashi-Hiroshima, 739, Japan
SO EMBO Journal (1997), 16(12), 3715-3723 CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English
AB Six copies of insertion elements accumulate in the subtelomeric region immediately proximal to the telomeric repeats on Chlorella chromosome I. The elements, designated Zepps, bear the characteristic features of non-viral (LINE-like) retrotransposons, including a ***poly*** (***A***) tail, 5'-truncations, a retroviral reverse transcriptase-like ORF and flanking target duplications. Detailed sequence anal. of the Chlorella subtelomeric region revealed a novel mechanism of Zepp transposition; successive insertions of each Zepp element into another Zepp as a target, leaving a tandem ***array*** of their 3'-regions with ***poly*** (***A***) tracts facing toward the centromere. Only the most distal Zepp copy was inverted to connect its ***poly*** (***A***) tail with the telomeric repeats. A similar Zepp cluster but without the telomeric repeats was also found at the terminus of another Chlorella chromosome. These structures contrast with that proposed for the addn. of HeT-A and TART elements to Drosophila telomeres. Expression of Zepp elements is induced by

heat shock treatment. Possible roles of the subtelomeric retrotransposons in formation and maintenance of telomeres are discussed.

L12 ANSWER 116 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:683966 CAPLUS <<LOGINID::20061115>>
DN 125:319520
TI Zepp, a LINE-like retrotransposon found in the Chlorella telomeres
AU Noutoshi, Yoshiteru; Higashiyama, Takanobu; Fujie, Makoto; Yamada, Takashi
CS Dep. Fermentation Technol., Hiroshima Univ., Higashi-Hiroshima, 739, Japan
SO Nucleic Acids Symposium Series (1996), 35(Twentythird Symposium on Nucleic Acids Chemistry, 1996), 305-306 CODEN: NACSD8; ISSN: 0261-3166
PB Oxford University Press
DT Journal
LA English
AB Several copies of insertion elements were found to be accumulated in the region adjacent to the telomeric repeats on Chlorella chromosome I. The elements, designated Zepps, bear the characteristic features of nonviral (LINE-like) retrotransposons including an ORF with homol. to retroviral reverse transcriptase, 5'-truncations, flanking target duplications, and the ***poly*** (***A***) tail. A novel mechanism of the Zepp transposition was revealed by detailed structural anal.: successive insertions of each Zepp element into another Zepp as a target, leaving a tandem ***array*** of their 3'-regions with ***poly*** (***A***) tracts facing toward the centromere. Possible roles of the subtelomeric retrotransposons in the formation and maintenance of telomeres are discussed.

L12 ANSWER 117 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:547103 CAPLUS <<LOGINID::20061115>>
DN 125:188593
TI Targeting and function in mRNA export of nuclear pore complex protein Nup153
AU Bastos, Ricardo; Lin, Amy; Enarson, Mark; Burke, Brian
CS Dep. Cell Biology, Harvard Medical School, Boston, MA, 02115, USA
SO Journal of Cell Biology (1996), 134(5), 1141-1156 CODEN: JCLBA3; ISSN: 0021-9525
PB Rockefeller University Press
DT Journal
LA English
AB Nup153 is a large (153 kDa) O-linked glycoprotein which is a component of the basket structure located on the nucleoplasmic face of nuclear pore complexes. This protein exhibits a tripartite structure consisting of a zinc finger domain flanked by large (60-70 kDa) NH2- and COOH-terminal domains. When full-length human Nup153 is expressed in BHK cells, it accumulates appropriately at the nucleoplasmic face of the nuclear envelope. Targeting information for Nup153 resides in the NH2-terminal domain since this region of the mol. can direct an ordinarily cytoplasmic protein, pyruvate kinase, to the nuclear face of the nuclear pore complex. Overexpression of Nup153 results in the dramatic accumulation of nuclear ***poly*** (***A***)+ RNA, suggesting an inhibition of RNA export from the nucleus. This is not due to a general decline in nucleocytoplasmic transport or to occlusion or loss of nuclear pore complexes since nuclear protein import is unaffected. While overexpression of certain Nup153 constructs was found to result in the formation of unusual intranuclear membrane ***arrays*** , this structural phenotype could not be correlated with the effects on ***poly*** (***A***)+ RNA distribution. The RNA trafficking defect was, however, dependent upon the Nup153 COOH-terminal domain which contains most of the XFXFG repeats. It is proposed that this region of Nup153, lying within the distal ring of the nuclear basket, represents a docking site for mRNA mols. exiting the nucleus.

L12 ANSWER 118 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:412585 CAPLUS <<LOGINID::20061115>>
DN 125:107809
TI Interrelationships of the pathways of mRNA decay and translation in eukaryotic cells
AU Jacobson, Allan; Peltz, Stuart W.
CS Dep. Mol. Genet. Microbiol., Univ. Massachusetts Med. Sch., Worcester, MA, 01655-0122, USA
SO Annual Review of Biochemistry (1996), 65, 693-739 CODEN: ARBOAW; ISSN: 0066-4154
PB Annual Reviews
DT Journal; General Review
LA English
AB A review, with 400 refs. While the potential importance of mRNA stability to the regulation of gene expression has been recognized, the structures and mechanisms involved in the detn. of individual mRNA decay rates have just begun to be elucidated, particularly in mammalian systems and yeast. It is now well established that mRNA decay is not a default process, in which an ***array*** of nonspecific nucleases degrades indiscriminately based on target size or ribosome protection of the substrate. Rather, like transcription, RNA processing, and translation, mRNA decay is a precise process dependent on a variety of specific cis-acting sequences and trans-acting factors. Entry into the pathways of mRNA decay is triggered by at least three types of initiating event: ***poly*** (***A***) shortening, arrest of translation at a premature nonsense codon, and endonucleolytic cleavage. Steps subsequent to ***poly*** (***A***) shortening or premature translational termination converge in a pathway that progresses from removal of the 5' cap to exonucleolytic digestion of the body of the mRNA. MRNA fragments generated by endonucleolytic cleavage are most likely removed by exonucleolytic decay as well, but these events have not been characterized in detail. Nucleases and other factors (including mRNA sequence elements and autoregulatory proteins) required for the promotion or inhibition of these pathways have been identified by both biochem. and genetic methods and systematic attempts to understand their resp. roles have begun. MRNA sequences whose presence or absence has marked effects on mRNA decay rates include the ubiquitous cap and ***poly*** (***A***) tail, sequences that comprise endonuclease cleavage sites, and sequences that promote ***poly*** (***A***) shortening. The latter are found in the 3'-UTR (untranslated region) and in coding regions. Evidence that ***poly*** (***A***) stimulates translation initiation, that some destabilization sequences must be translated to function, and that premature translation termination promotes rapid mRNA decay indicates a close linkage between the elements regulating mRNA decay and components of the protein synthesis app. This linkage, and other data, leads us to propose a model for a functional mRNP. In this model, interactions between factors assocd. with opposite ends of an mRNA stimulate translation initiation and minimize the rate of entry into the pathways of mRNA decay. Events that initiate mRNA decay are postulated to be those that can disrupt this functional complex and create substrates for exonucleolytic digestion.

L12 ANSWER 119 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:380954 CAPLUS <<LOGINID::20061115>>
DN 125:106773
TI Novel gene transcripts preferentially expressed in human muscles revealed by quantitative hybridization of a high density cDNA ***array***
AU Pietu, Genevieve; Alibert, Olivier; Guichard, V. alerie; Lamy, Bernard; Bois, Florence; Leroy, Elisabeth; Mariage-Samson, Regine; Houlgatte, Remi; Soularue, Pascal; Auffray, Charles
CS Genexpress, Centre National Recherche Scientifique, Evry, 91002, Fr.
SO Genome Research (1996), 6(6), 492-503 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB A set of 1091 human skeletal muscle cDNA clone inserts representing more than 800 human gene transcripts were spotted as PCR products at high d. on nylon membranes. Replicas of the filters were hybridized in stringent conditions with 33P-radiolabeled cDNA probes transcribed from skeletal muscle ***poly*** (***A***)+ RNA. Hybridization signals were collected on phosphor screens and processed using a software specifically adapted for this application to identify and quantitate each spot. Parameters likely to influence the hybridization signal intensity were assessed to eliminate artifacts. Each clone was assigned to one of four intensity classes reflecting the steady-state level of transcription of the corresponding gene in skeletal muscle. Differential expression of specific gene transcripts was detected using complex cDNA probes derived from nine different tissues, allowing assessment of their tissue specificity. This made is possible to identify 48 novel gene transcripts (including 7 homologous or related to known sequences) with a muscle-restricted pattern of expression. These results were validated through the anal. of known muscle-specific transcripts and by Northern anal. of a subset of the novel gene transcripts. All these genes have been registered in the Genexpress Index, such that sequence, map, and expression data can be used to decipher their role in the physiol. and pathol. of human muscles.

L12 ANSWER 120 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:81202 CAPLUS <<LOGINID::20061115>>
DN 124:199907
TI A region of 20 bp repeats lies 3' of human Ig C.alpha.1 and C.alpha.2 genes
AU Chen, Chaoqun; Birshtein, Barbara K.
CS Department Cell Biology, Albert Einstein College Medicine, Bronx, NY, 10461, USA
SO International Immunology (1996), 8(1), 115-22 CODEN: INIMEN; ISSN: 0953-8178
PB Oxford University Press
DT Journal
LA English
AB The murine Ig heavy chain gene locus is regulated by multiple elements. In addn. to the intron enhancer, E.mu., there is a complex regulatory region 3' of the C.alpha. gene, which spans .apprx.40 kb and contains several enhancers. In contrast to mouse, the human IgH cluster contains two C.alpha. genes, each assocd. with duplicated ***arrays*** of other CH genes. There is evidence to suggest that each ***array*** is individually regulated. In this report, the authors describe an .apprx.2 kb region contg. 20 bp repeats that lies 3' of both human C.alpha.1 and C.alpha.2 genes. This repeat region appears to be the site of integration of the Epstein-Barr virus in the RGN1 B lymphoma cell line. The repeat region is homologous to a 420 bp segment in mouse that is located downstream of the C.alpha. membrane exon in the interval preceding the second of three ***poly*** (***A***) termination sites. However, in contrast to human, the murine segment contains degenerate repeats. The human repeat region bears significant homol. to switch sequences, in particular to S.mu. and S.alpha.. The authors hypothesize that the human repeat regions may play a role in the class switch process by contributing to the stabilization of interactions between the two switch regions. The presence of a Sau3A site within the repeats presents a barrier to cloning with several existing human genomic libraries, most of which are based on partial Sau3A digestion. Furthermore, the homol. of the repeat region with S.mu. and S.alpha. sequences may contribute to the difficulty in isolating YAC clones contg. C.alpha. genes since homologous recombination could potentially have deleted this entire segment. The authors' map of these DNA segments provides a guide to their isolation and characterization.

L12 ANSWER 121 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:910098 CAPLUS <<LOGINID::20061115>>
DN 123:310040
TI Protein synthesis in Metarhizium anisopliae growing on host cuticle
AU Stleger, Raymond J.; Joshi, Lokesh; Bidochka, Michael J.; Roberts, Donald W.
CS Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, NY, 14853-1801, USA
SO Mycological Research (1995), 99(9), 1034-40 CODEN: MYCRER; ISSN: 0953-7562
PB Cambridge University Press
DT Journal
LA English
AB In vitro protein synthesis using ***poly*** (***A*** +)RNA and a two-step gel system for proteins were used in this study on the entomopathogenic fungus Metarhizium anisopliae to provide an est. of the magnitude of differential protein synthesis and secretion that may be involved in adapting to growth on insect cuticle. Shortly after being transferred to a media contg. cockroach cuticle, mRNAs for certain proteins are repressed while a broad ***array*** of mRNAs for other proteins is induced. Concurrent with this, a least 42 proteins were secreted into the media in a process which was sensitive to actinomycin D. The majority of these proteins were acidic (pI range 4.2-5.6) and co-migrated with Con-A/peroxidase stained bands, indicating that they might be glycoconjugates. Microsequencing of those polypeptides accumulated in large amts. revealed two NH2-terminal amino acid sequences from acidic proteins that were highly homologous to those of animal trypsins. The trypsin nature of the two proteins was confirmed using a combination of gelatin-SDS-polyacrylamide gel electrophoresis and enzyme overlay membranes. The NH2-terminal sequence of the major basic protein identified it as a known subtilisin-like proteinase (PrI). A second basic sequence was identified as a carboxypeptidase. No other homologies were found.

L12 ANSWER 122 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:819288 CAPLUS <<LOGINID::20061115>>
DN 123:247809
TI Differential gene expression in the murine thymus assayed by quantitative hybridization of ***arrayed*** cDNA clones

AU Nguyen, Catherine; Rocha, Dominique; Granjeaud, Samuel; Baldit, Mylene; Bernard, Karine; Naquet, Philippe; Jordan, Bertrand R.
CS Centre d'Immunologie, CNRS, Marselle, 13288, Fr.
SO Genomics (1995), 29(1), 207-16 CODEN: GNMCEP; ISSN: 0888-7543
PB Academic
DT Journal
LA English
AB High-throughput measurement of hybridization signatures obtained using complex probes prepd. from ***poly*** (***A***)+RNA and high-d. cDNA colony filters is described. The performance of the system, elimination of artifacts, and verification of the validity of the data are discussed. CDNAs corresponding to sequences present at levels of approx. 0.01% in the complex probe can be detected. Good correlation is obsd. between expression profiles detd. by this method and by Northern blotting. The method is applied to a preliminary investigation of differential expression in three cell types present in the murine thymus.

L12 ANSWER 123 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:396208 CAPLUS <<LOGINID::20061115>>
DN 123:2380
TI Molecular organization of Chlorella vulgaris chromosome I: presence of telomeric repeats that are conserved in higher plants
AU Higashiyama, Takanobu; Maki, Sinya; Yamada, Takashi
CS Dep. Fermentation Technol., Hiroshima Univ., Higashi-Hiroshima, 724, Japan
SO Molecular & General Genetics (1995), 246(1), 29-36 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer
DT Journal
LA English
AB The unicellular green alga Chlorella vulgaris (strain C-169) has a small genome (38.8 Mb) consisting of 16 chromosomes, which can be easily sepd. by CHEF gel electrophoresis. The authors have isolated and characterized the smallest chromosome (chromosome I, 980 kb) to elucidate the fundamental mol. organization of a plant-type chromosome. Restriction mapping and sequence analyses revealed that the telomeres of this chromosome consist of 5'-TTTAGGG repeats running from the centromere towards the termini; this sequence is identical to those reported for several higher plants. This sequence is reiterated .apprx.70-fold at both termini, although individual clones exhibited microheterogeneity in both sequence and copy no. of the repeats,. Subtelomeric sequences proximal to the termini were totally different from each other; on the left arm, unique sequence elements (14-20 bp) which were specific to chromosome I, form a repeat ***array*** of 1.7 kb, whereas a 1.0-kb sequence on the right arm contained a ***poly*** (***A***)-assocd. element immediately next to the telomeric repeats. This element is repeated several times on chromosome I and many times on all the other chromosomes of this organism.

L12 ANSWER 124 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:278259 CAPLUS <<LOGINID::20061115>>
DN 122:102015
TI Altered gene expression in thermoadapted cultured cells of cowpea.
AU Cherry, Joe H.; Mayer, Randall R.; Heuss-LaRosa, Kathleen; Reddy, P. Maheshwara; Singh, Narendra K.
CS Department of Botany and Microbiology, Auburn University, Auburn, AL, 36849-5407, USA
SO NATO ASI Series, Series H: Cell Biology (1994), 86(Biochemical and Cellular Mechanisms of Stress Tolerance in Plants), 229-42 CODEN: NASBE4; ISSN: 1010-8793
DT Journal
LA English
AB Suspension cell cultures of cowpea (Vigna unguiculata) were adapted to grow gradually at a normally non-permissive temp. of 38.degree.. Proteins expressed were compared to those of thermoadapted cells maintained at 38.degree. for >20 growth cycles, to those of unadapted cells maintained at 26.degree., and unadapted cells heat-shocked at 42.degree.. The expression of mRNAs, and differentially expressed cDNAs were also compared for each of these cultures. Unadapted cells transferred to an elevated temp. produced the normal ***array*** of heat shock proteins, while thermoadapted cells produced large nos. of proteins present in unadapted cells and several novel peptides not present in unadapted cells or heat-shocked cells. Twenty-six differentially expressed cDNA clones were isolated using subtracted probes from a cDNA library produced from mRNA isolated from thermoadapted cells. These clones represent 8 hybridization groups and 6 groups of cDNA clones exhibit increased level of gene expression in thermoadapted cells. These non-hsp genes are involved in the long-term tolerance to hyperthermic stress.

L12 ANSWER 125 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:13859 CAPLUS <<LOGINID::20061115>>
DN 122:73369
TI A Drosophila melanogaster chromosome 2L repeat is expressed in the male germ line
AU Russell, Steven R. H.; Kaiser, Kim
CS Dep. Genet., Univ. Cambridge, Cambridge, CB2 3EH, UK
SO Chromosoma (1994), 103(1), 63-72 CODEN: CHROAU; ISSN: 0009-5915
DT Journal
LA English
AB We describe the initial characterization of a Drosophila melanogaster locus, Mst40 (Male-specific transcript), that was cloned on the basis of its male-specific transcription during the third larval instar. Corresponding low mol. wt. ***poly*** (***A***)+ mRNAs are abundant in primary spermatocytes, but in no other larval or adult tissue. During early embryogenesis Mst40 expression is complex; initially transcription is detected during early cleavage stages. This early expression appears as two discrete dots of hybridization assocd. with each nucleus. Subsequently, the transcripts are abundant in the cytoplasm of the newly formed pole cells. In the genome Mst40 sequences are located in region 40, at the base of chromosome 2L, close to, or within, the .beta.-heterochromatin. The Mst40 sequences are organized as a tandemly ***arrayed*** 1.4 kb repeat unit. The repeat is conserved in all D. melanogaster strains examd. but absent from other Drosophila species studied. The locus does not correspond to any known complementation groups in the region and has yet to be assigned a function.

L12 ANSWER 126 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1994:580090 CAPLUS <<LOGINID::20061115>>
DN 121:180090
TI "Slim" nucleosides and nucleotides. I. Synthetic, structural and biophysical investigations of showdomycins
AU Mumper, Mary W.; Aurenge, CHristophe; Hosmane, Ramachandra S.

CS Department of Chemistry and Biochemistry, University of Maryland Baltimore County, Baltimore, MD, 21228, USA
SO Journal of Biomolecular Structure & Dynamics (1994), 11(5), 1107-31 CODEN: JBSDD6; ISSN: 0739-1102
DT Journal
LA English
AB A new, convenient, and short synthesis of 2'-deoxyshowdomycin, along with an improved procedure for the prepn. of showdomycin, have been presented. A single-crystal x-ray structure of 1-benzyl-2'-deoxyshowdomycin has been reported. Conformational studies using C.D. indicated that showdomycin exists predominantly in an anti conformation in aq. soln. Mol. mechanics calcns. using AMBER point to comparable binding energy of showdomycin-adenosine pair with the natural uridine-adenosine pair, but with a significant base-ribose conformational deviation from the natural ***array*** in the former. Implications of such a conformational deviation on tumor and viral replications have been discussed. Base-pairing studies employing high resoln. NMR spectroscopy indicates that both showdomycin and epishowdomycin base-pair with adenosine-5'-monophosphate (AMP); however, while showdomycin also show evidence of stacking, that was absent in epishowdomycin. Mol. modeling studies using QUANTA/CHARMm show that showdomycin is capable of forming a homopolymer duplex by base-pairing with ***poly*** (***A***), but with considerably broader and deeper major groove. A heteropolymer duplex with a single insert of showdomycin exhibits tighter coiling at the point of insertion. A ten-picosecond dynamics simulation of the above heteroduplex revealed relaxation of the helix with disruption of H-bonding for two base pairs on either side of the insertion point, forming a large central cavity.

L12 ANSWER 127 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1994:571902 CAPLUS <<LOGINID::20061115>>
DN 121:171902
TI Can SINEs: a family of tRNA-derived retroposons specific to the superfamily Canoidea
AU Coltman, David W.; Wright, Jonathan M.
CS Department of Biology, Dalhousie University, Halifax, NS, B3H 4J1, Can.
SO Nucleic Acids Research (1994), 22(14), 2726-30 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A repetitive element of approx. 200 bp was cloned from harbor seal (Phoca vitulina concolor) genomic DNA. The sequence of the element revealed putative RNA polymerase III control boxes, a ***poly*** ***A*** tail and direct terminal repeats characteristic of SINEs. Sequence and secondary structural similarities suggest that the SINE is derived from a tRNA, possibly tRNA-alanine. Southern blot anal. indicated that the element is predominately dispersed in unique regions of the seal genome, but may also be present in other repetitive sequences, such as tandemly ***arrayed*** satellite DNA. Based on slot-blot hybridization anal., the authors est. that 1.3.times.106 copies of the SINE are present in the harbor seal genome; SINE copy no. based on the no. of clones isolated from a size-selected library, however, is an order of magnitude lower (1-3.times.105 copies), an est. consistent with the abundance of SINEs in other mammalian genomes. Database searches found similar sequences have been isolated from dog (Canis familiaris) and mink (Mustela vison). These, and the seal SINE sequences are characterized by an internal CT dinucleotide microsatellite in the tRNA-unrelated region. Hybridization of genomic DNA from representative species of a wide range of mammalian orders to an oligonucleotide (30mer) probe complementary to a conserved region of the SINE confirmed that the element is unique to carnivores of the superfamily Canoidea.

L12 ANSWER 128 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1994:475189 CAPLUS <<LOGINID::20061115>>
DN 121:75189
TI An in vivo assay for the reverse transcriptase of human retrotransposon L1 in Saccharomyces cerevisiae
AU Dombroski, Beth A.; Feng, Qinghua; Mathias, Stephen L.; Sassaman, Donna M.; Scott, Alan F.; Kazazian, Haig H., Jr.; Boeke, Jef D.
CS Dep. Mol. Biol. Genet., Johns Hopkins University School Medicine, Baltimore, MD, 21205, USA
SO Molecular and Cellular Biology (1994), 14(7), 4485-92 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB L1 elements constitute a highly repetitive human DNA family (50,000 to 100,000 copies) lacking long terminal repeats and ending in a ***poly*** (***A***) tail. Some L1 elements are capable of retrotransposition in the human genome (Kazazian, H. H., Jr., C. Wong, H. Youssoufian, A. F. Scott, D. G. Phillips, and S. E. Antonarakis, Nature (London) 332:164-166, 1988). Although most are 5' truncated, a consensus sequence of complete L1 elements is 6 kb long and contains two open reading frames (ORFs) (Scott, A. F., B. J. Schmeckpepper, M. Abdelrazik, C. T. Comey, B. O'Hara, J. P. Rossiter, T. Cooley, P. Heath, K. D. Smith, and L. Margolet, Genomics 1:113-125, 1987). The protein encoded by ORF2 has reverse transcriptase (RT) activity in vitro (Mathias, S. L., A. F. Scott, H. H. Kazazian, Jr., J. D. Boeke, and A. Gabriel, Science 254:1808-1810, 1991). Because L1 elements are so numerous, efficient methods for identifying active copies are required. The authors have developed a simple in vivo assay for the activity of L1 RT based on the system developed by Derr et al. (Derr, L. K., J. N. Strathern, and D. J. Garfinkel, Cell 67:355-364, 1991) for yeast HIS3 pseudogene formation. L1 ORF2 displays an in vivo RT activity similar to that of yeast Ty1 RT in this system and generates pseudogenes with unusual structures. Like the HIS3 pseudogenes whose formation depends on Ty1 RT, the HIS3 pseudogenes generated by L1 RT are joined to TY1 sequences and often are part of complex ***arrays*** of Ty1 elements, multiple HIS3 pseudogenes, and hybrid Ty1/L1 elements. These pseudogenes differ from those previously described in that there are extra base pairs of unknown origin inserted at several of the junctions. In two of three HIS3 pseudogenes studied, the L1 RT appears to have jumped from the 5' end of the a Tyr1/L1 transcript to the ***poly*** (***A***) tract of the HIS3 RNA.

L12 ANSWER 129 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1993:666634 CAPLUS <<LOGINID::20061115>>
DN 119:266634
TI A comparison between the effects of benzyladenine and light on plastid development in excised watermelon cotyledons
AU Longo, C.; Marziani, G.; Rossi, G.; Bracale, M.
CS Dip. Biol., Univ. Milano, Milan, I-20133, Italy
SO Physiol. Biochem. Cytokinins Plants, Symp. (1992), Meeting Date 1990, 271-5. Editor(s): Kaminek, Miroslav; Mok, David W. S.; Zazimalova, Eva. Publisher: SPB Acad. Publ., The Hague, Neth. CODEN: 59KXA9
DT Conference
LA English

AB The effects of BA and light were compared on 2D-electrophoretic patterns, representing total plastid proteins, products of in vitro translation directed by total ***poly*** (***A***)-mRNA, and products of in organello protein synthesis by isolated plastids from watermelon cotyledons. Illumination and BA treatment induced a common set of polypeptides. The no. of common polypeptides induced by either treatment was greater than the no. of BA- or light-specific spots. In comparison with protein patterns from plastids of control cotyledons, light and BA greatly enhanced the no. and intensity of polypeptide spots. Analyses of translational products revealed, however, that control cotyledons contain a comparatively large ***array*** of mRNAs even in the absence of BA and light. It is reasonable to assume that a sizeable fraction of these messengers codes for plastid proteins. A similar result was obtained in the case of protein synthesis in organello, in that plastids from control cotyledons were able to synthesize a large no. of proteins. These two observations suggest that dark-grown cotyledons have the potential capability to synthesize a large no. of plastid proteins.

L12 ANSWER 130 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1993:464423 CAPLUS <<LOGINID::20061115>>
DN 119:64423
TI A procyclin-associated gene in Trypanosoma brucei encodes a polypeptide related to ESAG 6 and 7 proteins
AU Koenig-Martin, Elke; Yamage, Mat; Roditi, Isabel
CS Inst. Genet. Toxikol., Kernforschungszent. Karlsruhe, Karlsruhe, Germany
SO Molecular and Biochemical Parasitology (1992), 55(1-2), 135-45 CODEN: MBIPDP; ISSN: 0166-6851
DT Journal
LA English
AB The procyclin genes of T. brucei encode a family of glycoproteins expressed on the surface of procyclic forms of the parasite. These genes are present at different loci in tandem ***arrays*** of 2 or 3 copies depending on the strain. It has previously been shown that procyclin genes are transcribed from a promotor immediately upstream of the first procyclin gene in each cluster by an RNA polymerase that is resistant to high levels of .alpha.-amanitin. Addnl. genes, which the authors term procyclin-assocd. genes (PAGs), are located downstream of the procyclin genes and belong to the same .alpha.-amanitin-resistant polycistronic transcription units. A gene in the Pro A locus, PAG 1, encodes a polypeptide that is related to the ESAG 6 and 7 proteins encoded in the VSG expression site. An unexpected feature of PAG 1 is that the major open reading frame of 405 amino acids only starts at position 1283 in the cDNA sequence and extends to the ***poly*** (***A***) tail. Sequences related to the 5' untranslated region of PAG 1 are also found downstream of procyclin genes in other loci, but the 3' coding region is unique to Pro A. This suggests that there are related PAGs which are coordinately transcribed with procyclin genes from different loci.

L12 ANSWER 131 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1993:188368 CAPLUS <<LOGINID::20061115>>
DN 118:188368
TI A three-dimensional view of precursor messenger RNA metabolism within the mammalian nucleus
AU Carter, Kenneth C.; Bowman, Douglas; Carrington, Walter; Fogarty, Kevin; NcNeil, John A.; Fay, Fredric S.; Lawrence, Jeanne Bentley
CS Med. Cent., Univ. Massachusetts, Worcester, MA, 01655, USA
SO Science (Washington, DC, United States) (1993), 259(5099), 1330-5 CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB A quant. 3-dimensional anal. of nuclear components involved in precursor mRNA metab. was performed with a combination of fluorescence hybridization, immunofluorescence, and digital imaging microscopy. ***Poly*** (***A***) RNA-rich transcript domains were discrete, internal nuclear regions that formed a ventrally positioned horizontal ***array*** in monolayer cells. A dimmer, sometimes strand-like, ***poly*** (***A***) RNA signal was dispersed throughout the nucleoplasm. Spliceosome assembly factor SC-35 localized within the center of individual domains. These data support a nuclear model in which there is a specific topol. arrangement of noncontiguous centers involved in precursor mRNA metab., from which RNA transport toward the nuclear envelope radiates.

L12 ANSWER 132 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1992:167631 CAPLUS <<LOGINID::20061115>>
DN 116:167631
TI Sequence of the .gamma.2b membrane 3' untranslated region: ***polyA*** site determination and comparison to the .gamma.2a membrane 3' untranslated region
AU Ward, Susan B.; Morrison, Sherie L.
CS Columbia Univ., New York, NY, 10032, USA
SO Molecular Immunology (1992), 29(2), 279-85 CODEN: MOIMD5; ISSN: 0161-5890
DT Journal
LA English
AB Here the nucleotide sequence is presented of the .gamma.2b membrane 3' untranslated region as well as approx. 443 nucleotides of 3' flanking sequence. Although this region contains two potential polyadenylation hexanucleotides AATAAA (located 1328 and 1407 nucleotides downstream of the last membrane exon), it appears that only the first site directs polyadenylation of the mature mRNA. The first AATAAA is followed by several sequences which may influence its relative strength: the region downstream of this AATAAA is 44% T-rich and contains a pair of CAYTG sequences (4/5 match) which overlap two sequences which have a 6/8 match to the sequence YGTGTTYY. These sequences have been found in proximity to a large no. of 3' ends. The AATAAA site at position 1407 is not flanked by a T- or GT-rich sequence and is followed by a single CAYTG sequence (4/5 match) and a single YGTGTTYY sequence (6/8 match). The region downstream of the second AATAAA site also contains a sequence which has an 8/12 match with a sequence found in all heavy chain secreted 3' untranslated regions. Consistent with sequence comparisons between other regions of these two genes, the .gamma.2b sequence has striking homol. with the .gamma.2a 3' untranslated region. A notable difference between .gamma.2b and .gamma.2a is the absence of an extensive ***array*** of GAA, GA, GGAA, and GGA repeats from the .apprx.2b sequence. The GA repeats are postulated to form a stem loop structure in the .gamma.2a 3' untranslated region; .gamma.2b then would be missing the 5' half of the stem. Interestingly, neither the .gamma.2b nor the .gamma.2a 3' untranslated regions show large homologies to the .mu., .delta., .gamma.3, or the .alpha. membrane 3' untranslated regions.

L12 ANSWER 133 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1992:103913 CAPLUS <<LOGINID::20061115>>
DN 116:103913

TI Specificity of the immune response to the group B polysaccharide of Neisseria meningitidis
AU Lifely, M. R.; Esdaile, J.
CS Dep. Exp. Immunobiol., Wellcome Biotech, Beckenham/Kent, BR3 3BS, UK
SO Immunology (1991), 74(3), 490-6 CODEN: IMMUAM; ISSN: 0019-2805
DT Journal
LA English
AB A panel of monoclonal antibodies (mAb) and polyclonal sera of murine, human, and equine origin, of IgM isotype and with specificity for N. meningitidis group B polysaccharide, an .alpha.(2 .fwdarw. 8)-linked homopolymer of sialic acid, were examd. for their antigenic and biol. specificities. The nature of the antigenic determinants on B polysaccharide was investigated using a series of N-acyl derivs. of B polysaccharide, 2 sialic acid polymers contg. .alpha.(2 .fwdarw. 9)-linkages, and a series of polynucleotides. The panel of antibodies recognized an ***array*** of unrelated antigenic determinants on the B polysaccharide, despite its structural simplicity, and all but one were highly effective in an in vitro bactericidal assay and/or in an in vivo murine passive protection model. There was no evidence that B polysaccharide induced antibody capable of blocking biol. activity (blocking antibody).

L12 ANSWER 134 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1991:578095 CAPLUS <<LOGINID::20061115>>
DN 115:178095
TI Two novel protein-tyrosine kinases, each with a second phosphotransferase-related catalytic domain, define a new class of protein kinase
AU Wilks, Andrew F.; Harpur, Ailsa G.; Kurban, R. R.; Ralph, Stephen J.; Zuercher, Gisela; Ziemiecki, Andrew
CS Ludwig Inst. Cancer Res., R. Melbourne Hosp., Melbourne, 3050, Australia
SO Molecular and Cellular Biology (1991), 11(4), 2057-65 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The protein tyrosine kinases (PTKs) are a burgeoning family of proteins, each of which bears a conserved domain of 250-300 amino acids capable of phosphorylating substrate proteins on tyrosine residues. Recently, the existence of 2 highly conserved sequence elements within the catalytic domain was exploited to generate PTK-specific degenerate oligonucleotide primers. By application of the polymerase chain reaction, portions of the catalytic domains of several novel PTKs were amplified. Here, the primary sequence is reported of one of these new PTKs, JAK1 (from Janus kinase), a member of a new class of PTK characterized by the presence of a 2nd phosphotransferase-related domain immediately N-terminal to the PTK domain. The sequence was derived from the cDNA sequence of a human fibroblast clone. The 2nd phosphotransferase domain bears all the hallmarks of a protein kinase, although its structure differed significantly from that of the PTK and threonine/serine kinase family members. A 2nd member of this family (JAK2) was partially characterized and exhibited a similar ***array*** of kinase-related domains. JAK1 is a large, widely expressed membrane-assocd. phosphoprotein of .apprx.130 kDa. The PTK activity of JAK1 was located in the C-terminal PTK-like domain. The role of the 2nd kinase-like domain is unknown.

L12 ANSWER 135 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1991:442899 CAPLUS <<LOGINID::20061115>>
DN 115:42899
TI Maturation of polycistronic pre-mRNA in Trypanosoma brucei: analysis of trans splicing and ***poly*** (***A***) addition at nascent RNA transcripts from the hsp70 locus
AU Huang, Jin; Van der Ploeg, Lex H. T.
CS Coll. Phys. Surg., Columbia Univ., New York, NY, 10032, USA
SO Molecular and Cellular Biology (1991), 11(6), 3180-90 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB Numerous protein-coding genes of the protozoan T. brucei are arranged in tandem ***arrays*** that are transcribed polycistronically. The pre-mRNA transcripts are processed by trans splicing, leading to the addn. of a capped 39-nucleotide (nt) miniexon and by ***poly*** (***A***) addn. The authors wished to det. the order of the RNA processing events at the hsp70 locus and address the potential occurrence of cotranscriptional RNA processing. The rate of transcriptional elongation at the hsp70 locus in isolated nuclei measured between 20 and 40 nt/min. This low rate of RNA chain elongation allowed the authors to label the 3' end of hsp70 nascent RNA with a short (about 180-nt) 32P tail. The structure of the labeled nascent hsp70 RNA could then be analyzed by RNase T1 and RNase T1/RNase A mapping. The trans splicing of hsp70 pre-mRNA did not occur immediately after the synthesis of the 3' splice acceptor site, and nascent RNA mols. that contained about 550 nt of RNA beyond the 3' splice acceptor site still had not acquired a miniexon. In contrast, nascent RNA with a 5' end that mapped to the polyadenylation site of the hsp70 genes could be detected, indicating that maturation of the pre-mRNA in trypanosomes involves a rapid cleavage of the nascent hsp70 RNA (within seconds after synthesis of the site) for ***poly*** (***A***) addn. The data suggest that polycistronic pre-mRNA is unlikely to be synthesized in toto and rather appears to be processed cotranscriptionally by cleavage for ***poly*** (***A***) addn.

L12 ANSWER 136 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1990:230596 CAPLUS <<LOGINID::20061115>>
DN 112:230596
TI A transcriptional analysis of the Trypanosoma brucei hsp83 gene cluster
AU Mottram, Jeremy C.; Murphy, William J.; Agabian, Nina
CS Univ. California, San Francisco, CA, USA
SO Molecular and Biochemical Parasitology (1989), 37(1), 115-27 CODEN: MBIPDP; ISSN: 0166-6851
DT Journal
LA English
AB Ten to twelve copies of the 83-kDa heat-shock protein gene (hsp83) from T. brucei are arranged in a head-to-tail tandem ***array*** of 2.8-kb repeat units, which are transcribed to give 2.6-kb mature mRNAs. One of the repeat units was cloned and sequenced. The gene encodes a putative protein of 81 kDa which is highly homologous to Hsp83 of Drosophila melanogaster (75%), Hsp90 of Saccharomyces cerevisiae (72%), and the C62.5 protein of Escherichia coli (61%). The 5' end of the mature mRNA was mapped by primer extension sequence anal. and shown to contain the spliced leader. The mapping of the 3'-***poly*** (***A***) addn. sites by S1 anal. indicated that there is a 218-nucleotide (nt) intergenic sequence linking the boundaries encoding the mature mRNA. Within this sequence are a no. of elements conserved with the trypanosome hsp70 intergenic region, including a 14-nt sequence that also has homol. to the Drosophila heat-shock consensus element.

L12 ANSWER 137 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1990:113229 CAPLUS <<LOGINID::20061115>>
DN 112:113229
TI The gene of the yeast ribosomal protein L32
AU Dabeva, M.; Warner, J. R.
CS Inst. Cell Biol. Morphol., Sofia, Bulg.
SO Metab. Enzymol. Nucleic Acids Incl. Gene Manipulations, [Proc. Int. Symp.], 6th (1988), Meeting Date 1987, 203-12. Editor(s): Zelinka, Jan; Balan, Jozef. Publisher: Plenum, New York, N. Y. CODEN: 56OGAP
DT Conference
LA English
AB The genes for ribosomal proteins rP29 and rPL32 occur in a head-to-head ***array*** in Saccharomyces cerevisiae. The sequence of the rP29 gene was previously reported. In this report the sequence of the rPL32 gene is presented. The gene contains a single 230-bp-long intron which is located immediately after the first AUG codon. S1 nuclease mapping and primer extension anal. revealed only one major transcription initiation site at position -58. S1 nuclease mapping and sequencing of the 3' ends of the 2 cDNA clones revealed that the ***poly*** (***A***) tract starts at nucleotide 648 downstream from the first codon. The coding region of the gene conforms exactly with that of the cDNA clones. The amino acid sequence was detd. for rPL32 which is moderately basic compared with other rP. The N-terminal portion is highly basic, whereas the C-terminal portion is nearly neutral. The sequence of the intergenic region between the rP29 and rPL32 genes was detd. A search for common sequences located upstream of most rP genes revealed the presence of some homologous sequences, but none of these were perfect matches. The intergenic region was similar in length (.apprx.600 nucleotides) to that located between the rPL46 and rPS24 genes. Both intergenic regions contain a centrally located RPG-box and other common sequences. Two rPL32-LacZ fusion plasmids were used to det. that the consensus sequence HOMOLI and the RPG-box on the coding strand of rP29 have an important role in expression of the rPL32 gene, although their deletion did not abolish the background transcription of the gene. Deletion anal. revealed that at least 220 nucleotides upstream of the TATA box were required for transcription of the rPL32 gene.

L12 ANSWER 138 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1989:434647 CAPLUS <<LOGINID::20061115>>
DN 111:34647
TI Expression and tissue-specific assembly of human butyrylcholine esterase in microinjected Xenopus laevis oocytes
AU Soreq, Hermona; Seidman, Shlomo; Dreyfus, Patrick A.; Zevin-Sonkin, Dina; Zakut, Haim
CS Life Sci. Inst., Hebrew Univ., Jerusalem, 91904, Israel
SO Journal of Biological Chemistry (1989), 264(18), 10608-13 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Cholinesterases represent a ubiquitous, polymorphic family of acetylcholine hydrolyzing enzymes. The multileveled tissue-specific heterogeneity which characterizes these enzymes makes the cholinesterases an appropriate model for studying the mechanisms involved in regulating divergent pathways in protein biogenesis. For this purpose, a cDNA coding for human butyrylcholine esterase (BuChE) was subcloned into the SP 6 transcription vector. Synthetic mRNA transcribed from this construct was microinjected into X. laevis oocytes alone, and in conjunction with ***poly*** (***A***)+ RNAs extd. from human brain or muscle. Injected BuChE-mRNA induced the biosynthesis of a protein exhibiting the catalytic activity, substrate specificity, and sensitivity to selective inhibitors characteristic of native human serum BuChE, and clearly distinct from the related enzyme acetylcholinesterase (AChE). The nascent BuChE was reproducibly distributed into low salt-sol. and detergent-extractable pools. Sucrose gradient anal. demonstrated that the nascent human enzyme was capable of limited subunit assembly, appearing as functional dimeric mols. in both of these fractions. Co-injection with brain or muscle-derived mRNAs facilitated higher order oligomeric assembly. Co-injected brain mRNA induced the appearance of tetramers while co-injected muscle mRNA induced the appearance of an ***array*** of heavy mol. forms, including a heavy 16 S form. These results indicate that the mol. determinants which distinguish BuChE from AChE are inherent to its primary amino acid sequence and that addnl., tissue-specific protein(s) are involved in the modulation of subunit assembly within particular biol. milieues.

L12 ANSWER 139 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1989:70435 CAPLUS <<LOGINID::20061115>>
DN 110:70435
TI Mulcos: a vector for amplification and simultaneous expression of two foreign genes in mammalian cells
AU Ikeda, Hitoshi; Trowsdale, John; Saito, Izumu
CS Human Immunogenet. Lab., Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SO Gene (1988), 71(1), 19-27 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A method was developed for amplification and expression of foreign genes in mammalian cells. This procedure exploits the fact that an SfiI cleavage site, GGCCGCCT/CGGCC (the recognition sequences are underlined), is present at the SV40 replication origin and the cleaved ends, CCT-3' and AGG-3', are not rotationally equiv. Thus DNA fragments flanked by the SfiI sites can be ligated in head-to-tail tandem ***arrays*** and cloned in cosmids; the resulting construct is called a mulcos. The cosmid vector, pCHD21, contains the single SfiI site as well as HmBR and dhfr genes which are selectable markers in mammalian cells. Cassette plasmid pmoRH contains 2 expression units, each of which consists of SV40 early promoter, EcoRI or HindIII cloning site, small T splicing region, and ***poly*** (***A***) signal, and the 2 units as a whole are flanked by the SfiI sites. A set of .alpha.- and .beta.-chain cDNAs of a human major histocompatibility class-II antigen were inserted into the EcoRI and HindIII sites, resp. The purified SfiI fragment, contg. both expression units, was then ligated with SfiI-linearized cosmid vector pCHD2L at a molar ratio of 20:1. A mulcos contg. 8 pairs of the .alpha.- and .beta.-chain expression units was isolated by in vitro packaging in phage .lambda. heads and subsequent transfection into Escherichia coli. Drug-selected mouse cells transfected with the mulcos contained significantly higher copy nos. of the expression units and higher expression levels than those obtained using conventional plasmids. More than 85% of these cells expressed class-II antigen on their cell surfaces. These results showed that the method described here offers simultaneous expression of two genes in a cell without the necessity for selection by a fluorescence-activated cell sorter.

L12 ANSWER 140 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1989:70273 CAPLUS <<LOGINID::20061115>>

DN 110:70273
TI A related moderately repetitive DNA family in the nematodes Ascaris lumbricoides and Panagrellus silusiae
AU Warren, T.; Pasternak, J. J.
CS Dep. Biol., Univ. Waterloo, Waterloo, ON, N2L 3G1, Can.
SO Nucleic Acids Research (1988), 16(22), 10833-47 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Digestion of genomic DNA from the nematodes P. silusiae and A. lumbricoides with restriction endonuclease BamHI releases a 0.7 kilobase (kb) fragment. The 0.7 kb fragment from both nematodes was cloned onto Escherichia coli plasmid pUC19. Using representative clones as DNA hybridization probes, it was found that (1) the BamHI fragments cross-hybridize; (2) a ladder-effect with multiples of 0.7 kb was evident in both species after hybridization to genomic DNA; and (3) the genomic copy no. of BamHI elements is 150 and 195 for P. silusiae and A. lumbricoides, resp. DNA sequence anal. of the inserts AL700-1 and PS700-1 revealed nucleotide blocks with >85% similarity. No open reading frames are present in either DNA fragment. Neither fragment hybridizes to genomic DNA from Caenorhabditis elegans. Northern blot hybridization indicated that the 0.7 kb element is transcribed into ***poly*** (***A***)- RNA in P. silusiae but is not transcribed in adult Ascaris muscle. Thus, P. silusiae and A. lumbricoides share a homologous, tandemly ***arrayed*** , moderately repetitive DNA family.

L12 ANSWER 141 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1988:567909 CAPLUS <<LOGINID::20061115>>
DN 109:167909
TI Proteins regulating actin assembly in oogenesis and early embryogenesis of Xenopus laevis: gelsolin is the major cytoplasmic actin-binding protein
AU Ankenbauer, Thomas; Kleinschmidt, Juergen A.; Vandekerckhove, Joel; Franke, Werner W.
CS Inst. Cell Tumor Biol., German Cancer Res. Cent., Heidelberg, D-6900, Fed. Rep. Ger.
SO Journal of Cell Biology (1988), 107(4), 1489-98 CODEN: JCLBA3; ISSN: 0021-9525
DT Journal
LA English
AB Oocytes, notable those of amphibia, accumulate large pools of nonfilamentous (sol.) actin, both in the cytoplasm and in the nucleoplasm, which coexist with extensive actin filament ***arrays*** in the cytoplasmic cortex. Because the regulation of oogenically accumulated actin is important in various processes of oogenesis, egg formation, fertilization, and early embryogenesis, the major actin-binding proteins present in oocytes of X. laevis were purified and characterized. The major actin-binding component in the ooplasm, but not in the nucleus, is a polypeptide of Mr .apprx.93,000 on SDS-PAGE that reduces actin polymn. in vitro in a Ca2+-dependent manner but promotes nucleation events, and also reduces the viscosity of actin polymers, indicative of severing activity. Antibodies were raised against the purified oocyte protein, and it is different from villin, is also prominent in unfertilized eggs and early embryos, is very similar to a corresponding protein present in various tissues and in cultured cells, and appears to be spread over the cytoplasm. By using these antibodies a cDNA clone was isolated from a .lambda.gt11 expression library of ovarian ***poly*** (***A***)+-RNA. Detn. of the amino acid sequence derived from the nucleotide sequence, together with the directly detd. sequence of the amino terminus of the native protein, showed that this clone encodes the C-terminal half of gelsolin. Thus, gelsolin is the major actin-modulating protein in oogenesis and early embryogenesis of amphibia, and probably also of other species, that probably also plays an important role in the various Ca2+-dependent gelation and contractility processes characteristic of these development stages.

L12 ANSWER 142 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1988:544944 CAPLUS <<LOGINID::20061115>>
DN 109:144944
TI Ribonucleoproteins package 700 nucleotides of pre-mRNA into a repeating ***array*** of regular particles
AU Conway, Greg; Wooley, John; Bibring, Thomas; LeStourgeon, Wallace M.
CS Dep. Mol. Biol., Vanderbilt Univ., Nashville, TN, 37235, USA
SO Molecular and Cellular Biology (1988), 8(7), 2884-95 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB An assay for the in vitro assembly of HeLa cells 40 S heterogeneous nuclear ribonucleoprotein particles (hnRNP particles) was developed. The substrates were single-stranded nucleic acid polymers of defined length and sequence prepd. in vitro and the 6 major core particle proteins from isolated 40 S hnRNP. The fidelity of in vitro assembly was evaluated on various phys. parameters, including sedimentation, salt dissocn., polypeptide stoichiometry, UV-activated protein-RNA crosslinking, and overall morphol. Correct particle assembly depended on RNA length and on the input protein/RNA ratio but not on the concn. of the reactant mixt. nor on the presence or absence of internal RNA processing signals, a 5'-cap structure, a 3'- ***poly*** (***A***) moiety, or ATP as energy source. RNA lengths of 685-726 nucleotides supported correct particle assembly. Dimers and oligomeric complexes that possessed the same polypeptide stoichiometry as native hnRNP assembled on RNA chains that were integral multiples of 700 nucleotides. Intermediate-length RNA supported the assembly of nonstoichiometric complexes lacking structural homogeneity. An anal. of these complexes indicates that proteins A1 and A2 may be the first proteins to bind RNA during particle assembly. Thus, the major proteins of 40 S hnRNP particles contg. the necessary information for packaging nascent transcripts into a repeating ribonucleosomal structure possessing a defined RNA length and protein compn. but do not themselves contain the information for modulating packaging that may be required for RNA splicing.

L12 ANSWER 143 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1988:404125 CAPLUS <<LOGINID::20061115>>
DN 109:4125
TI Isolation and characterization of fibroin mRNAs from the saturniid silkworms, Antheraea yamamai, Antheraea pernyi and Philosamia cynthia ricini
AU Tamura, T.; Sakate, S.
CS Seric. Exp. Stn., Tsukuba, 305, Japan
SO Insect Biochemistry (1988), 18(2), 169-75 CODEN: ISBCAN; ISSN: 0020-1790
DT Journal
LA English
AB Fibroin mRNAs of the saturniid silkworms, A. yamamai, A. pernyi, and P. cynthia ricini, were isolated and characterized. First, the total cellular RNAs of the posterior silk glands of the saturniid larvae at the wandering stage were extd. by the SDS-phenol method. Then, the high-mol.-wt. RNA was isolated by Sepharose 2B column chromatog. and sucrose-gradient centrifugation. These high-mol.-wt. RNAs were detd. to be the

fibroin mRNAs of the saturniid silkworms based on the following characteristics: (1) each RNA prepn. displayed a single band in an agarose gel and its mol. wt. detd. by the gel agreed with the expected size calcd. from each fibroin polypeptide; (2) these RNAs contained 60% G + C (guanine + cytosine) as expected since the fibroins contain large amts. of glycine and alanine, whose codons are GGX and GCX, resp.; and (3) the RNAs bound to an oligo d(T) column, indicating that the RNAs possess a ***poly*** ***A*** tail, and were translated into an ***array*** of polypeptides by a rabbit reticulocyte lysate.

L12 ANSWER 144 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1988:32918 CAPLUS <<LOGINID::20061115>>
DN 108:32918
TI Multiple copies of a retroposon interrupt spliced leader RNA genes in the African trypanosome, Trypanosoma gambiense
AU Aksoy, Serap; Lalor, Thomas M.; Martin, Jennifer; Van der Ploeg, Lex H. T.; Richards, Frank F.
CS Sch. Med., Yale Univ., New Haven, CT, 06510, USA
SO EMBO Journal (1987), 6(12), 3819-26 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB The 140-nucleotide spliced leader (SL) RNA, involved in mRNA maturation in the African trypanosomes and in other kinetoplastida, is encoded by a tandem ***array*** of spliced leader genes. The 1.4-kb SL gene repeat unit in T. gambiense is organized in tandem ***arrays*** confined to two large (min. size, 350-450 kb) restriction fragments. SL genes in both ***arrays*** are interrupted by a total of eight conserved insertion elements. Cleavage of genomic DNA at restriction sites present within the insertion element, but not in the SL gene repeat, releases variable nos. of SL genes from the tandem ***array*** . Since the insertion element contains a terminal ***poly*** (***A***) track of 36 bases and because a 49-bp duplication of target DNA has occurred at the integration site, it is concluded that it is a retroposon. This retroposon is uniquely assocd. with the SL gene clusters. These retroposons presumably originated from a single insertion event after which their copy no. increased, possibly through unequal sister chromatid exchange.

L12 ANSWER 145 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1987:132855 CAPLUS <<LOGINID::20061115>>
DN 106:132855
TI Tandemly arranged gene clusters of malarial parasites that are highly conserved and transcribed
AU Vaidya, Akhil B.; Arasu, Prema
CS Dep. Microbiol. Immunol., Hahnemann Univ., Philadelphia, PA, USA
SO Molecular and Biochemical Parasitology (1987), 22(2-3), 249-57 CODEN: MBIPDP; ISSN: 0166-6851
DT Journal
LA English
AB A mol. clone contg. a 5.8-kb EcoRI fragment was isolated from a genomic library of the rodent malarial parasite Plasmodium yoelii. The P. yoelii genome contains about 150 copies of this sequence, making up almost 3% of the DNA. These sequences are tandemly ***arrayed*** in head-to-tail configurations with the unit length of the repeat being 5.8 kb. Several ***poly*** (***A***)+ RNAs of P. yoelii ranging from 1.6 to 0.3 kb are recognized by the 5.8-kb clone. Five addnl. species of malarial parasites (P. chabaudi, P. berghei, P. falciparum, P. knowlesi, and P. cynomolgi) contain tandemly repeated ***arrays*** of sequences having the same unit length of 5.8 kb, which readily hybridie to the sequence cloned from P. yoelii.

L12 ANSWER 146 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1986:528755 CAPLUS <<LOGINID::20061115>>
DN 105:128755
TI The expression and genomic organization of randomly selected cloned Drosophila melanogaster genes
AU Goldstein, Elliott S.; Vincent, Walter S.; Schultz, Kathleen A.
CS Zool. Dep., Arizona State Univ., Tempe, AZ, 85287, USA
SO Biochimica et Biophysica Acta, Gene Structure and Expression (1986), 867(4), 209-19 CODEN: BBGSD5; ISSN: 0167-4781
DT Journal
LA English
AB A lambda recombinant DNA library contg. D. melanogaster nuclear DNA inserts was screened with cDNA made from oocyte and gastrula ***poly*** (***A***)+ RNA. A total of 124 clones were isolated which represented sequences complementary to a distribution of abundancies of their RNAs. The clone set was then used as probes to identify those whose RNA abundancies changed during embryonic development. The vast majority of clones showed little difference during development. Four different clones were identified whose ***poly*** (***A***)+ RNAs were quant. regulated; 2 were oocyte-specific, and 2 were embryonic-specific. Forty-four clones were chosen for in-situ hybridization to salivary gland polytene chromosomes. The location and distribution of their sites are described. A class of clones, identified by in-situ hybridization to the nucleolus, is further described. These clones contain a scrambled ***array*** of ribosomal intervening sequences.

L12 ANSWER 147 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1986:528586 CAPLUS <<LOGINID::20061115>>
DN 105:128586
TI A single gene from yeast for both nuclear and cytoplasmic polyadenylate-binding proteins: domain structure and expression
AU Sachs, Alan B.; Bond, Martha W.; Kornberg, Roger D.
CS Sch. Med., Stanford Univ., Stanford, CA, 94305, USA
SO Cell (Cambridge, MA, United States) (1986), 45(6), 827-35 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB Nuclear and cytoplasmic ***poly*** (***A***)-binding proteins were purified from Saccharomyces cerevisiae, and antisera were used to isolate a gene that encodes them. The gene occurs in a single copy on chromosome 5 and gives rise to a unique, unspliced 2.1-kb transcript. The nuclear protein appears to be derived from the cytoplasmic one by proteolytic cleavage into 53- and 17-kd polypeptides that remain assocd. during isolation. DNA sequence detn. reveals 4 tandemly ***arrayed*** 90-amino acid regions of homol. that probably represent ***poly*** (***A***)-binding domains. A 55-residue A-rich region upstream of the initiator methionine codon in the mRNA shows an affinity for ***poly*** (***A***)-binding protein comparable to that of ***poly*** (***A***)180-220, raising the possibility of feedback regulation of translation.

L12 ANSWER 148 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1986:436423 CAPLUS <<LOGINID::20061115>>
DN 105:36423

TI 4.5S RNA is encoded by hundreds of tandemly linked genes, has a short half-life, and is hydrogen bonded in vivo to ***poly*** (***A***)-terminated RNAs in the cytoplasm of cultured mouse cells
AU Schoeniger, Luke O.; Jelinek, Warren R.
CS Med. Cent., New York Univ., New York, NY, 10016, USA
SO Molecular and Cellular Biology (1986), 6(5), 1508-19 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The 4.5 S RNA is a group of RNAs 90 to 94 nucleotides long (length polymorphism due to a varying no. of UMP residues at the 3' end) that form hydrogen bonds with ***poly*** (***A***)-terminated RNAs isolated from mouse, hamster, or rat cells. A gene was cloned that encodes the 4.5 S RNA. It is repeated 850 (.sigma. = 54) time/haploid mouse genome and 690 (.sigma. = 59) times/haploid rat genome. Most, if not all, of the repeates in both species are ***arrayed*** in tandem. The repeat units is 4245 base pairs (bp) long in mouse DNA (the complete base sequence of 1 repeat units is presented) and .apprx. 5300 bp in rat DNA. This accounts for .apprx.3 .times. 106 bp of genomic DNA in each species, or 0.1% of the genome. Cultured murine erythroleukemia cells contain 13,000 mol./cell of the 4.5 S RNA, which can be labeled to equil. in 90 min by [3H]uridine added to the culture medium. The 4.5 S RNA, therefore, has a short half-life. The 4.5 S RNA can be crosslinked in vivo by 4'-aminomethyl-4,5',8-trimethylpsoralen to murine erythroleukemia cell ***poly*** (***A***)-terminated cytoplasmic RNA contained in ribonucleoprotein particles.

L12 ANSWER 149 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1984:401816 CAPLUS <<LOGINID::20061115>>
DN 101:1816
TI Molecular cloning of cDNA for Avena phytochrome
AU Hershey, Howard P.; Colbert, James T.; Lissemore, James L.; Barker, Richard F.; Quail, Peter H.
CS Dep. Bot., Univ. Wisconsin, Madison, WI, 53706, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1984), 81(8), 2332-6 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Several cDNA clones were isolated for phytochrome, a plant regulatory photoreceptor. A cDNA library was constructed by using etiolated Avena ***poly*** (***A***)+ RNA enriched for phytochrome mRNA by size fractionation. Replicate ***arrays*** of colonies were differentially screened with cDNA probes made from ***poly*** (***A***)+ RNA that had been either enriched in or depleted of phytochrome mRNA. Of the colonies hybridizing preferentially with the enriched probe, several contained plasmids that specifically selected phytochrome mRNA when assayed by hybridization-selection and translation. The largest such plasmid, pAP-2, was used to isolate clones from an Avena genomic library. One of these genomic clones was then used to screen a 2nd cDNA library in an attempt to identify full-length phytochrome clones. The largest of the plasmids thus obtained, pAP-3, contains a 3.4-kilobase-pair (kbp) insert, verified to contain phytochrome sequences by hybridization-selection and translation. Sequence anal. of pAP-2 and pAP-3 revealed that the 2 clones are identical in sequence through a 2.4-kbp region in which they overlap. However, the pAP-2 insert contains, in addn., 1.5 kbp of sequence of unknown origin, the apparent result of a recombination event. Blots of ***poly*** (***A***)+ RNA hybridized with 32P-labeled pAP-2 or pAP-3 show a single mRNA band at 4.2 kilobases. Blot anal. of RNA from dark-grown and from red-irradiated tissue demonstrates that a previously reported light-induced decrease in translatable phytochrome mRNA results from a decrease in phys. abundance of this mRNA.

L12 ANSWER 150 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:195541 CAPLUS <<LOGINID::20061115>>
DN 98:195541
TI De novo synthesis and specific assembly of keratin filaments in nonepithelial cells after microinjection of mRNA for epidermal keratin
AU Kreis, Thomas E.; Geiger, Benjamin; Schmid, Erika; Jorcano, Jose L.; Franke, Werner W.
CS Dep. Chem. Immunol., Weizmann Inst. Sci., Rehovot, 76100, Israel
SO Cell (Cambridge, MA, United States) (1983), 32(4), 1125-37 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB ***Poly*** (***A***)-contg. RNA isolated from bovine muzzle epidermis was microinjected into nonepithelial cells contg. only intermediate-sized filaments of the vimentin type. In recipient cells, keratin polypeptides are synthesized and assemble into intermediate-sized filaments at multiple dispersed sites. The time course and the pattern of de novo assembly of keratin filaments was described within living cells. These filaments were indistinguishable, by immunofluorescence and immunoelectron microscopic criteria, from keratin filament ***arrays*** present in true epithelial cells. The presence of extended keratin fibril meshworks in these injected cells is compatible with cell growth and mitosis. Double immunolabeling revealed that newly assembled keratin was not codistributed with microfilament bundles, microtubules, or vimentin filaments. Possibly mechanisms exist which in vivo sort out newly synthesized cytokeratin polypeptides from vimentin.

L12 ANSWER 151 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:175450 CAPLUS <<LOGINID::20061115>>
DN 98:175450
TI Reverse transcriptase and its associated ribonuclease H: interplay of two enzyme activities controls the yield of single-stranded cDNA
AU Berger, Shelby L.; Wallace, Donald M.; Puskas, Robert S.; Eschenfeldt, William H.
CS Lab. Pathophysiol., Natl. Cancer Inst., Bethesda, MD, 20205, USA
SO Biochemistry (1983), 22(10), 2365-72 CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The synthesis of single-stranded globin cDNA by the RNA-directed DNA polymerase activity of reverse transcriptase (I) of avian myeloblastosis virus in the presence of oligo(dT) primers was investigated in order to det. the limitations to higher yields. The assocd. RNase H activity, an integral part of I, plays a large role in the synthesis of the 1st strand of cDNA and the interplay of the 2 enzyme activities for any specific set of conditions dets. the yield of single-stranded products. In both the presence and the absence of polymn., the assocd. RNase H catalyzed the deadenylylation of mRNA, producing mols. that were somewhat shorter, highly homogeneous in size, and fully translatable into globin. They were also entirely lacking in the ability to serve as templates for cDNA synthesis. The reaction was completely dependent on oligo(dT) and completely independent of deoxyribonucleoside triphosphates. The initial rate of

deadenylylation was 25% of the initial rate of initiation of polymn. when satg. levels of deoxyribonucleoside triphosphates were used in the polymerase reaction. In the presence of RNase H activity, the DNA polymerase catalyzed the synthesis of an ***array*** of cDNAs including some that were full length. The initiation of polymn. was rate-limiting; once synthesis had begun, it required 1-1.5 min to transcribe globin mRNA. However, most primers that were elongated were aborted prematurely. Max. synthesis of full-length cDNA required stoichiometric levels of enzyme and high triphosphate levels, but regardless of conditions, the sum of completed cDNA and deadenylylated mRNA accounted for only 50% of the input mRNA. The data fit a model in which synthesis of full-length cDNA mols. depends on the arrangement of primers and transcription initiation complexes on the ***poly*** (***A***) tail of mRNA.

L12 ANSWER 152 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:102055 CAPLUS <<LOGINID::20061115>>
DN 98:102055
TI Molecular cloning of cDNA sequences for avian malic enzyme. Nutritional and hormonal regulation of malic enzyme mRNA levels in avian liver cells in vivo and in culture
AU Winberry, Larry K.; Morris, Sidney M., Jr.; Fisch, Judith E.; Glynias, Manuel J.; Jenik, Robert A.; Goodridge, Alan G.
CS Dep. Pharmacol., Case West. Reserve Univ., Cleveland, OH, 44106, USA
SO Journal of Biological Chemistry (1983), 258(2), 1337-42 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB A double-stranded cDNA library constructed from the total ***poly*** (***A*** +) RNA of goose uropygial gland was screened for recombinants contg. sequences complementary to malic enzyme (I) [9028-47-1] mRNA. Replicate ***arrays*** of 1400 colonies were hybridized independently with 32P-labeled cDNAs copied from 2 populations of hepatic RNA derived from tissues which differed by .apprx.35-fold with respect to the relative synthesis of I. Of the colonies which gave differential signals, 48 were further screened by hybrid-selected translation. DNA from 1 of these contained an insert of 970 base pairs and selected an mRNA which directed I synthesis in a cell-free system. The I sequences were subcloned into the single-stranded bacteriophage M13mp8. The subclones were used to prep. 32P-labeled single-stranded hybridization probes. Northern anal. indicated that I mRNA from both goose and chicken is .apprx.2100 bases in length. Hepatic I mRNA concn. is stimulated .gtoreq.30-50-fold when neonatal chicks or goslings, resp., are fed for 24 h. When added to chicken embryo hepatocytes in culture, triiodothyronine [6893-02-3] stimulated I mRNA accumulation by >100-fold. glucagon [9007-92-5] Inhibited the thyroid hormone-stimulated accumulation of I mRNA by 99%. In all instances, I mRNA concn. was closely correlated with the relative rate of I synthesis. Apparently, nutritional and hormonal regulation of I synthesis occurs at the pretranslational level.

L12 ANSWER 153 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:28724 CAPLUS <<LOGINID::20061115>>
DN 98:28724
TI Simple repeat sequence in Epstein-Barr virus DNA is transcribed in latent and productive infections
AU Heller, Mark; Van Santen, Vicky; Kieff, Elliott
CS Dep. Med., Univ. Chicago, Chicago, IL, 60637, USA
SO Journal of Virology (1982), 44(1), 311-20 CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB The BamHI K region of Epstein-Barr virus DNA is transcribed in latently infected cells from Burkitt tumors and in growth-transformed B-lymphocytes latently infected with Epstein-Barr virus. The nucleotide sequence of a 1153-base pair HinfI fragment in BamHI fragment K from the B95-8 Epstein-Barr virus isolate was detd. The fragment contains a remarkable 708-base pair simple sequence repeat ***array*** , designated IR3, which is composed of only 3 nucleotide triplet elements: GGG, GCA, and GGA. The triplets are organized into 3 repeat units: GCAGGA, GCAGGAGGA, and GGGGCAGGA. Immediately 3 of IR3 are tandem nearly perfect direct repeats of 2 different 24-base pair sequences. IR3 is conserved at a colinear position in the DNAs of other Epstein-Barr virus isolates, and a homologous sequence maps at the same location in the genome of a genetically related baboon herpesvirus, herpesvirus papio. IR3 is transcribed from left to right in latently infected, growth-transformed IB4 cells. It encodes part of a 2.0-kilobase exon of the 3.7-kilobase cytoplasmic polyadenylated RNA previously detected in IB4 cells. IR3 also encodes parts of 2.4- and 1.0-kilobase RNAs in productively infected B95-8 cells.

L12 ANSWER 154 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1982:50346 CAPLUS <<LOGINID::20061115>>
DN 96:50346
TI Anti- ***poly*** (***A***) polymerase antibodies in serums of tumor-bearing rats and human cancer patients
AU Stetler, Dean A.; Rose, Kathleen M.; Jacob, Samson T.
CS Milton S. Hershey Med. Cent., Pennsylvania State Univ., Hershey, PA, 17033, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1981), 78(12), 7732-6 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB ***Poly*** (***A***) polymerase (EC 2.7.7.19) was covalently linked to diazobenzyloxymethyl-filters and used to screen the sera from a no. of tumor-bearing rats and human cancer patients for antibodies to ***poly*** (***A***) polymerase. Sera from rats that had been inoculated with any of several Morris hepatomas or a mammary adenocarcinoma contained Igs capable of complexing with ***poly*** (***A***) polymerase. No antibodies to the enzyme could be detected in sera from control animals or from those bearing tumors for short periods of time. Antibodies to ***poly*** (***A***) polymerase were also obsd. in sera from human patients with leukemia, polycythemia vera, and Wilms' tumor. The antibodies were not evident in sera from normal volunteers or from patients with nonneoplastic diseases including lupus erythematosus, a disorder in which antibodies are produced against an ***array*** of nuclear proteins. Igs from the serum of 1 of the human patients were capable of inhibiting ***poly*** (***A***) polymerase activity in vitro, whereas those prepd. from the serum of a normal volunteer did not affect enzyme activity. As detd. by the diazobenzyloxymethyl-filter technique, the relative concn. of antibodies in the sera of an individual with leukemia (in remission) increased several-fold during a relapse. The presence of antibodies to ***poly*** (***A***) polymerase may be characteristic of sera from cancer patients and the relative concn. of these antibodies may be indicative of the disease state.

L12 ANSWER 155 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1980:404370 CAPLUS <<LOGINID::20061115>>
DN 93:4370
TI Construction of a cloned library of expressed embryonic gene sequences from Xenopus laevis
AU Dworkin, Mark B.; Dawid, Igor B.
CS Natl. Cancer Inst., NIH, Bethesda, MD, 20205, USA
SO Developmental Biology (Orlando, FL, United States) (1980), 76(2), 435-48 CODEN: DEBIAO; ISSN: 0012-1606
DT Journal
LA English
AB Total X. laevis ***poly*** (***A***)-contg. RNA from embryos at stage 10 (early gastrulae) and stage 41 (tadpoles) was copied into double-stranded complementary DNA (cDNA), inserted into plasmid pBR322 by poly(dA:dT) tailing, and introduced into Escherichia coli. Recombinant DNA libraries were obtained consisting of 5000 clones derived from stage 10 ***poly*** (***A***)-contg. RNA and 12,500 clones from stage 41 ***poly*** (***A***)-contg. RNA. At random 860 clones were selected for anal. by colony hybridization with cDNA-32P prepd. from stage 10 and stage 41 ***poly*** (***A***)-contg. RNA populations. About 20% of the clones gave a detectable hybridization signal with the homologous probe. Reconstruction expts. indicated than any clone contg. a sequence present at a level of .apprx.0.06% in the cDNA-32P probe can be detected. ***Poly*** (***A***)-contg. RNA from stage 10 embryos was dominated by a few very prominent sequences, whereas stage 41 ***poly*** (***A***)-contg. RNA was characterized by a larger ***array*** of less abundant species. With the colony hybridization method, the developmental behavior of a large no. of abundant RNA sequences can be evaluated.

L12 ANSWER 156 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1980:74170 CAPLUS <<LOGINID::20061115>>
DN 92:74170
TI Immunochemical study of the structure of ***poly*** (***adenylic*** acid)
AU Kahana, Zvi E.; Erlanger, Bernard F.
CS Inst. Cancer Res., Columbia Univ., New York, NY, 10032, USA
SO Biochemistry (1980), 19(2), 320-4 CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB Antibodies sp. for ***poly*** (***adenylic*** acid) (I) were generated by immunization of rabbits with I covalently linked to bovine serum albumin via the 3'-terminal residue of the polynucleotide. The antibodies pptd. with I as well as with nucleotide-protein conjugates, regardless of the purine or pyrimidine base, but not with conjugates of nucleosides. Pptn. was also seen with DNA and RNA and with polyribose phosphate. Agglutination of Hemophilus influenzae type b, which has a capsule of polyribose phosphate, was also demonstrated. In a competitive binding assay, the antibodies bound I with an affinity .gtoreq.4 orders of magnitude greater than that of oligo(adenylic acid) as large as A10. Cross-reaction was seen with poly(I), poly(C), poly(G), and polyribose phosphate. Unlike antibodies generated by I complexed with albumin, the specificity of these antibodies was directed at ribose phosphate residues, suggesting a conformation of I in soln. in which the purine residues are stacked inside a single-stranded helix with the ribose phosphate residues extending outward. This conformation is apparently disrupted by noncovalent complexing with albumin. I can thus be envisaged as a dense cloud of neg. charges arranged in a helical ***array*** . There is evidence that the conformation of I in RNA is the same; therefore, any theory for the role of the I tail in mRNA should take into account the contribution of a highly neg. charged segment at the 3' end.

L12 ANSWER 157 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1979:588098 CAPLUS <<LOGINID::20061115>>
DN 91:188098
TI Wheat embryo ribonucleates. XIV. Mass isolation of mRNA from wheat germ and comparison of its translational capacity with that of mRNA from imbibing wheat embryos
AU Cuming, A. C.; Kennedy, T. D.; Lane, B. G.
CS Biochem. Dep., Univ. Toronto, Toronto, ON, M5S 1A8, Can.
SO Canadian Journal of Biochemistry (1979), 57(9), 1170-5 CODEN: CJBIAE; ISSN: 0008-4018
DT Journal
LA English
AB Com. milled wheat germ is a convenient source material for facile recovery of mass (milligram) quantities of highly purified ***poly*** (***A***)-rich RNA. This ***poly*** (***A***)-rich RNA is efficiently translated in a nuclease-treated ext. of rabbit reticulocytes. By sucrose d. gradient fractionation of bulk ***poly*** (***A***)-rich RNA from wheat germ, it was possible to show that there is a direct relation between the mol. wts. of the polypeptide products of cell-free synthesis and the mol. wts. of the wheat mRNA mols. which program their synthesis. As assessed by Na dodecyl sulfate-polyacrylamide gel electrophoresis, the same ***array*** of polypeptides is synthesized when nuclease-treated reticulocyte ext. is programmed by ***poly*** (***A***)-rich RNA from either com. supplied or lab.-prepd. wheat embryos. Significantly, there are gross quant. if not qual. differences between the translational capacities of ***poly*** (***A***)-rich RNA from dry and imbibing wheat embryos, and the possible importance of these differences for interpreting a changing pattern of polypeptide synthesis in imbibing wheat embryos is the subject of a brief discussion.

L12 ANSWER 158 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1979:571758 CAPLUS <<LOGINID::20061115>>
DN 91:171758
TI Protein synthesis in imbibing wheat embryos
AU Cuming, Andrew C.; Lane, Byron G.
CS Dep. Biochem., Univ. Toronto, Toronto, ON, M5S 1A8, Can.
SO European Journal of Biochemistry (1979), 99(2), 217-24 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB Polypeptides synthesized by imbibing wheat embryos were compared with those made by cell-free exts. programmed with bulk ***poly*** (***A***)-rich RNA from dry, wheat embryos. Newly synthesized polypeptides, labeled with methionine-35S, were resolved by 1-dimensional and 2-dimensional electrophoresis and then records of the sepns. were prepd. by fluorog. When programmed by bulk ***poly*** (***A***)-rich RNA from dry wheat embryos, a nuclease-treated rabbit reticulocyte lyzate synthesized an ***array*** of polypeptides which is broadly similar to that formed when a wheat germ ext. is programmed with the same RNA. Polypeptides made in both homologous and heterologous cell-free systems, under the direction of bulk ***poly*** (***A***)-rich RNA from dry wheat embryos, were broadly similar to those formed during early (0-40 min) imbibition of dry

wheat embryos. As imbibition progressed beyond 40 min, there were profound changes in the 1- and 2-dimensional electrophoretic distributions of newly made polypeptides present in the 23,000 .times. g supernatant fraction of cell-free homogenates; characteristically, low-mol.-wt. and basic polypeptides comprised a diminishing proportion of the total polypeptides as imbibition progressed beyond 40 min. Ribosomal proteins were conspicuous among the proteins formed during early imbibition and esp. prominent among the products formed when homologous cell-free polypeptide synthesis was programmed by bulk ***poly*** (***A***)-rich RNA from dry wheat embryos.

L12 ANSWER 159 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1979:470143 CAPLUS <<LOGINID::20061115>>
DN 91:70143
TI Translational efficiency of cytoplasmic nonpolysomal messenger ribonucleic acid from sea urchin embryos
AU Rudensey, Lyle M.; Infante, Anthony A.
CS Biol. Dep., Wesleyan Univ., Middletown, CT, 06457, USA
SO Biochemistry (1979), 18(14), 3056-63 CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB Messenger RNA was isolated from polysomes and the free cytoplasmic nonpolysomal ribonucleoprotein particles (free RNPs or informosomes) of sea urchin embryos. These RNA populations were examd. for their capacities to direct protein synthesis in both the rabbit reticulocyte and wheat germ cell-free amino acid incorporation systems, pretreated with micrococcal nuclease to reduce endogenous incorporation. At equiv. concns. of each RNA, the rate of protein synthesis was greater with the templates from polysomes, and the maximal rate (Vmax) at satg. levels of RNA was .apprx.2-3 times greater for polysomal mRNA compared with the free RNP mRNA. Expts. using mixts. of the two ***poly*** (***A***) mRNA populations at nonsatg. levels showed that the difference in amino acid incorporation is not due to the presence of inhibitors in the free RNP RNA. The ability of each class of RNA to form 80 S initiation complexes was measured through ribosome binding studies. The free RNP mRNA has a 20% lower capacity to bind ribosomes, suggesting that these nonpolysomal mRNA mols. are enriched for inefficient initiators of protein synthesis relative to the templates present in polysomes. However, a specific subset of mRNAs (the 9 S histone mRNA) isolated from either the polysomes or free RNPs was equiv. in its ability to form 80 S initiation complexes. The difference in efficiency to be translated between the polysomal and nonpolysomal ***poly*** (***A***) mRNA does not appear to lie in the structures of the 5'-termini, since the translation of both classes of mRNA is inhibited to the same extent with a cap analog. Gel anal. of in vitro translation products revealed that the free RNPs and polysomes contain a similar highly complex ***array*** of messages. However, several major quant. differences in the pattern of translation products exist. Differences in the inherent abilities of various messages to be translated are suggested as an important means of regulating the ***array*** of proteins synthesized in an embryo during development.

L12 ANSWER 160 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1978:594269 CAPLUS <<LOGINID::20061115>>
DN 89:194269
TI A novel arrangement of tandemly repeated genes at a major heat shock site in D. melanogaster
AU Lis, John T.; Prestidge, Louise; Hogness, David S.
CS Dep. Biochem., Stanford Univ. Sch. Med., Stanford, CA, USA
SO Cell (Cambridge, MA, United States) (1978), 14(4), 901-19 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB Three cloned segments of Drosophila melanogaster DNA derived from the major heat shock site at 87.degree. in chromosome 3 were isolated. Each of these segments contained sequences homologous to a class of polysomal ***poly*** (***A***)-contg. RNAs whose synthesis was induced by heat shock of cultured cells. A combination of R loop, heteroduplex, and restriction fragment maps of these segments revealed that their homologous sequences are arranged in tandemly repeated units, each unit consisting of an .alpha. element (0.49 k-bases (kb)) joined to a .beta. element (1.10 kb). Polysomal RNAs homologous to these .alpha..beta. units (1.59 kb) were distributed into 3 size classes exhibiting approx. lengths of 1, 2, and 3 kb. R loop mapping demonstrated that the sequence of the 2-kb RNA is .alpha..beta..alpha., indicating that it, and presumably the 3-kb RNA, derive from transcripts covering >1 repeated unit. One of the cloned segments contained a variant repeat unit, .alpha..gamma., located between 2 .alpha..beta. units. This unit had the same .alpha. element, but the .beta. element was replaced by a nonhomologous .gamma. element (0.87 kb). Anal. of the total D. melanogaster DNA indicated that the 87.degree. locus contains .gtoreq.21 tandemly repeated units, distributed among .gtoreq.3 different tandem ***arrays*** sepd. by different spacer regions, 1 of which is within a cloned segment.

L12 ANSWER 161 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1975:599109 CAPLUS <<LOGINID::20061115>>
DN 83:199109
TI Monte-Carlo calculation of photon-initiated electromagnetic showers in lead glass
AU Longo, Egidio; Sestili, Ignazio
CS Ist. Fis. "G. Marconi", Univ. Rome, Rome, Italy
SO Nuclear Instruments & Methods (1975), 128(2), 283-307 CODEN: NUIMAL; ISSN: 0029-554X
DT Journal
LA English
AB. The results are presented of a Monte Carlo calcn. of the longitudinal and lateral development of photon-initiated electron-photon cascades in SF5 lead glass for the following energies of the primary photon: 100, 300, 500, 700, 1000, and 5000 MeV. The longitudinal development was carefully treated and a satisfactory anal. representation is suggested as a convenient tool for many practical problems. The lateral spread was analyzed and estd. from different points of view. Fluctuations obtained from the Monte Carlo calcn. for the track length of showers within 5, 10, and 15X0 of SF5 are presented. They were also obtained for an ***array*** of 9 counters - each 1 .times. X0 thick - placed one behind the other. These results were interpolated rather accurately with a ***Polya*** distribution for a convenient set of values of the corresponding parameters.

L12 ANSWER 162 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1970:38746 CAPLUS <<LOGINID::20061115>>
DN 72:38746
TI Representation of macromolecules and polymers of biological importance
AU Cohn, Waldo E.

CS Oak Ridge Nat. Lab., Oak Ridge, TN, USA
SO Journal of Chemical Documentation (1969), 9(4), 235-41 CODEN: JCHDAN; ISSN: 0021-9576
DT Journal
LA English
AB The structural anal. of natural polymers-proteins, polysaccharides, and nucleic acids has progressed to the point where long sequences, > 100 in many cases, of nonidentical monomeric units can be accurately positioned. Since even the accepted trivial names of the amino acids, monosaccharides, and nucleotides derived by hydrolysis, and thus considered to be the base units of the polymers, are too long for this situation, 3- or 1-letter contractions are employed in horizontal ***arrays*** . Known sequences are indicated by hyphens representing peptide, glycoside, or phosphodiester links, and unknown ones by commas between residues. Substitution on functional groups other than those in the linear main chain are symbolized by vertical bonds at the appropriate symbols. These conventions for the natural polymers have been extended to the polynucleotides recently synthesized by chem. and enzymic means, where homopolymers, repeating copolymers, and interchain assocns. are encountered. The source-based name, "polymer of," is reduced to either the prefix "poly" or the subscript suffix "n" (e.g., ***poly*** ***A*** or An). Known and random sequences in copolymers utilize the hyphen and comma, resp. [e.g., (A-U)n and (A,U)n]. Interchain assocn. (noncovalent) is shown by the center dot [as in (A)n.cntdot.(U)m], nonassocn. by a plus sign [(A)n + (G)m], and indefiniteness by a comma between the symbols defining each chain.

L12 ANSWER 163 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1967:43797 CAPLUS <<LOGINID::20061115>>
DN 66:43797
TI Effects of pressure on the helix-coil transitions of the ***poly*** ***adenylic*** acid-poly uridylic acid system
AU Hughes, Floyd; Steiner, Robert F.
CS Naval Med. Res. Inst., Bethesda, MD, USA
SO Biopolymers (1966), 4(10), 1081-90 CODEN: BIPMAA; ISSN: 0006-3525
DT Journal
LA English
AB The influence of hydrostatic pressure on the denaturation (helix-coil transitions) of 2- and 3-strand helices made from poly(riboadenylic acid) (***poly*** ***A***) and poly(ribouridylic acid (poly U) were tested and moderate pressure did not affect the width of the thermal profile of the transition. In the case of ***poly*** (***A*** + 2 U) the absorbance-pressure relation was nonlinear above 400 atm., and at 900 atm. .vdelta.A270/.vdelta.P changed signs, suggesting a process with a pos. vol. change. Over a pressure cycle, the absorbance showed hysteresis effects. Values obtained for the coil form indicated that the expt. is not sensitive enough to observe pressure effects on neutral ***poly*** ***A*** structure. The method is also unsuitable for transitions which are not readily reversible near the transition temp. Tm. The measured vol. change for ***poly*** (***A*** + U) may be considered as a valid thermodynamic parameter within certain limits, although the ordered and disordered phases are multicomponent systems of polymer, electrolyte, and preferentially bound water. The helix stability of the ***poly*** (***A*** + U) may be due to the release during melting of the adenine- and uracil units from their stacked ***array*** in the helix, with a breaking of the hydrophobic bonds, causing a decrease in vol. The breaking of adenine-uracil H bonds and partial or complete replacement of base bonding with solvent bonding will lead to an increased amt. of preferentially bound water, while alteration of the spatial relation of the charged phosphate groups will change their interaction with the electrolyte and solvent. Thus, the magnitude of the exptl. vol. change indicates an approx. balance at the Tm. 25 references.

L12 ANSWER 164 OF 164 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1961:131331 CAPLUS <<LOGINID::20061115>>
DN 55:131331
OREF 55:24772d-i,24773a-b
TI Optical rotatory properties of polynucleotides and nucleic acids
AU Fresco, J. R.
CS Harvard Univ.
SO Tetrahedron (1961), 13, 185-97 CODEN: TETRAB; ISSN: 0040-4020
DT Journal
LA Unavailable
AB cf. CA 51, 16629a. The optical rotatory effects observed in nucleic acids and polynucleotides were described and discussed. It was predicted that for a completely disordered polynucleotide chain of either the ribonucleic or deoxyribonucleic acid type the [.alpha.]D will be in the neighborhood of 0.degree.. In polynucleotides, a conformational effect might be expected to result from the helical ***array*** of the base pairs, which may be thought of as a series of discs translating about 36.degree. every 3-4 A. along the helix axis. The contribution due to these chromophores could, in fact, be quite large, if as might be supposed, the base pairs involve one or more n .fwdarw. .pi.* transitions in addn. to .pi. .fwdarw. .pi.* transitions. In an attempt to assess the contribution of helical conformation to rotatory power, the changes in specific rotation induced thermally in several helical polynucleotides was plotted along with optical density data. The plots showed that optical rotation was dependent on conformation, that at high temp. [.alpha.]D approached 0.degree. as predicted, and that the contribution due to helical conformation was sizable and pos., suggesting that all helices whose screw sense has been independently established must be right-handed. Comparison of the specific rotation of a multistrand helix [***poly*** (***A*** + A), [.alpha.]22D 300.degree., ***poly*** (***A*** + U), [.alpha.]22D 300.degree.] with its polyribonucleotide components (poly U-single strand, [.alpha.]22D -8.degree., ***poly*** ***A*** -single strand, [.alpha.]22D 155.degree.) showed that when the poly U strand assumed a helical conformation it contributed as high a pos. rotation as the ***poly*** ***A*** chain. The variation in specific rotation at 589 m.mu. and optical density at 257 m.mu. with the temp. of neutral solns. of ***poly*** ***A*** single strands led to the conclusion that nearly all H-bonded bases of single-stranded polynucleotides were contained within helical regions. From observations over the range 320-600 m.mu., it was evident that the rotatory properties of nucleosides are dominated by the base linked to the pentose and it was surmised that nucleotides will be found to display Cotton effects in the 230-300 m.mu. region. Examn. of polyriboadenylic acid was limited to the region 360-600 m.mu. and within this range, regardless of the conformation of the polynucleotide, all the data fitted the one-term Drude equation. The rotatory dispersion of ribonucleic acid followed the Drude equation regardless of the helical content. The rotatory dispersion of native deoxyribonucleic acid was delineated accurately in the 320-600 region and the changes accompanying denaturation examd. The dispersion was of the simple Drude type, but became anomalous

below 360 m.mu.. The anomaly was evidently related to the well-defined Cotton effect below 300 m.mu.. The observed Cotton effect was markedly displaced and diminished on denaturation. Both the red shift on denaturation and its location suggested that the effect was due to a n .fwdarw. .pi.* transition and it was presumed that other Cotton effects of the .pi. .fwdarw. .pi.* type of greater magnitude may exist in the near ultraviolet region. Native nucleic acids were later shown to contain closely spaced Cotton effects due to n .fwdarw. .pi.* and .pi. .fwdarw. .pi.* transitions. The differential sensitivity to naturations which the 2 types of electronic transitions exhibit in both ribonucleic and deoxyribonucleic acids was considered indicative of the differential influence of H-bonding between bases and the stacking of base pairs in helical polynucleotides.

=> d his
(FILE 'HOME' ENTERED AT 16:22:08 ON 15 NOV 2006)
FILE 'CAPLUS' ENTERED AT 16:22:29 ON 15 NOV 2006
L1 479 S (HYBRIDI?(20A)NANOPARTICLE#)/BI,AB
L2 20113 S ((POLYA) OR (POLY(W)A) OR (POLY(W)ADENYL?))/BI,AB
L3 2 S L1 AND L2
L4 156423 S ARRAY?/BI,AB
L5 44879 S MICROARRAY?/BI,AB
L6 191121 S L4 OR L5
L7 420 S L2 AND L6
L8 2 S L1 AND L7
L9 326 S L7 NOT 2006/PY
L10 255 S L9 NOT 2005/PY
L11 205 S L10 NOT 2004/PY
L12 164 S L11 NOT 2003/PY
L13 0 S L8 NOT L3
L14 59588 S SANDWICH?/BI,AB
L15 0 S L12 AND L14

=> log y
COST IN U.S. DOLLARS SINCE FILE
TOTAL ENTRY SESSION
FULL ESTIMATED COST 508.54 508.75

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE TOTAL ENTRY SESSION
CA SUBSCRIBER PRICE -124.50 -124.50

STN INTERNATIONAL LOGOFF AT 16:31:36 ON 15 NOV 2006